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OM protein - protein search, using sw model

Run on: April 2, 2003, 14:48:15 ; Search time 28 seconds
(Without alignments)
270.060 Million cell updates/sec

Title: US-10-002-278-9
Perfect score: 1368
Sequence: 1 DVIIDSETWDQATGKTFLV.....GVPTLKHYEGMSVAECGR 257

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
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3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
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6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Freq. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1368	100.0	257	4	US-08-065-844A-9
2	1336.5	97.7	428	1	US-08-050-132A-2
3	1336.5	97.7	428	3	US-08-750-222A-2
4	1336.5	97.7	428	3	US-08-815-652B-2
5	1336.5	97.7	428	4	US-08-254-353A-2
6	1336.5	97.7	428	5	PCT-US92-05374A-2
7	1336.5	97.7	428	5	PCT-US95-07084-2
8	808.5	59.1	427	4	US-08-065-844A-2
9	634	46.3	150	3	US-08-050-132A-9
10	634	46.3	150	3	US-08-815-652B-9
11	634	46.3	150	4	US-08-750-222A-9
12	634	46.3	150	4	US-08-254-353A-9
13	634	46.3	150	5	PCT-US92-05374A-9
14	634	46.3	150	5	PCT-US95-07084-9
15	519.5	38.0	312	1	US-08-247-908A-2
16	519.5	38.0	312	1	US-08-453-942-2
17	519.5	38.0	312	2	US-08-926-885A-2
18	519.5	38.0	312	5	PCT-US94-05290-2
19	516.5	37.8	424	1	US-08-247-908A-11
20	516.5	37.8	424	1	US-08-453-942-11
21	516.5	37.8	424	5	US-08-926-885A-11
22	516.5	37.8	424	5	PCT-US94-05290-11
23	469	34.3	103	1	US-08-335-583C-53
24	469	34.3	103	3	US-08-478-087A-15
25	469	34.3	103	4	US-08-931-858E-168
26	469	34.3	103	4	US-08-981-739-168
27	469	34.3	103	4	US-09-128-026-168

28	349.5	25.5	321	1	US-08-362-670B-26	Sequence 26, Appl
29	349.5	25.5	321	3	US-08-333-576C-26	Sequence 26, Appl
30	349.5	25.5	321	4	US-08-808-324-26	Sequence 26, Appl
31	349.5	25.5	321	5	PCT-US94-14030A-26	Sequence 26, Appl
32	348.5	25.5	417	1	US-08-199-780-1	Sequence 1, Appl
33	348.5	25.5	417	2	US-08-316-650-1	Sequence 1, Appl
34	348.5	25.5	417	5	PCT-US95-02251-1	Sequence 1, Appl
35	345	25.2	408	1	US-07-841-646-7	Sequence 7, Appl
36	345	25.2	408	1	US-07-718-274A-6	Sequence 6, Appl
37	345	25.2	408	1	US-07-901-703-19	Sequence 19, Appl
38	345	25.2	408	1	US-08-149-106-6	Sequence 6, Appl
39	345	25.2	408	1	US-08-147-023-7	Sequence 7, Appl
40	345	25.2	408	1	US-08-298-021-6	Sequence 6, Appl
41	345	25.2	408	1	US-08-050-132A-4	Sequence 4, Appl
42	345	25.2	408	1	US-08-447-570-7	Sequence 7, Appl
43	345	25.2	408	2	US-08-449-346-11	Sequence 11, Appl
44	345	25.2	408	2	US-08-448-700-7	Sequence 7, Appl
45	345	25.2	408	2	US-07-989-847-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-065-844A-9
Sequence 9, Application US/08065844A
Patent No. 633168
GENERAL INFORMATION:
APPLICANT: Jessell, Thomas M.
APPLICANT: Basler, Konrad
TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF
TITLE OF INVENTION: DORSALIN-1
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/065,844A
FILING DATE: 19930520
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28, 678
REFERENCE/DOCKET NUMBER: 0576/40314
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 664-0525
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UT
INFORMATION FOR SPO ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-065-844A-9
Query Match 100.0%; Score 1368; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVLDESETMDATGKTFELVSQDIRDEGWEETLEVSASVRRWRADSTTNKKNLEVTYOSH 60
| | | | |
Db 1 DVLDESETMDATGKTFELVSQDIRDEGWEETLEVSASVRRWRADSTTNKKNLEVTYOSH 60
QY 61 RESCOTLIDISVPSSKNLPFFVYVSNDRSNGTETRLDLKEMIGHBOETMLVKTAKNAY 120
| | | | |
Db 61 RESCOTLIDISVPSSKNLPFFVYVSNDRSNGTETRLDLKEMIGHBOETMLVKTAKNAY 120
QY 121 OGAGESOESEGLDGYTAVGPLRLARRKSTGASSHCQTSIRVNFEDIGDMSWIIAPKEYD 180
| | | | |
Db 121 OGAGESOESEGLDGYTAVGPLRLARRKSTGASSHCQTSIRVNFEDIGDMSWIIAPKEYD 180
QY 181 AVECKGGEFFPLADVPPTKHAIVQTLVHLKFPYKGAACVPTKSPISILYKDDMGVP 240
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Db 181 AVECKGGEFFPLADVPPTKHAIVQTLVHLKFPYKGAACVPTKSPISILYKDDMGVP 240
QY 241 TLKYHEGMSVAECGCR 257
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Db 241 TLKYHEGMSVAECGCR 257

RESULT 2

US-08-050-132A-2
; Sequence 2, Application US/08050132A
; Patent No. 5661007
; GENERAL INFORMATION:
; APPLICANT: Wozney, John M.
; APPLICANT: Celeste, Anthony
; TITLE OF INVENTION: BMP-9 COMPOSITIONS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: Legal Affairs - 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: US
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/050,132A
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kapinos, Ellen J.
; REGISTRATION NUMBER: 32,245
; REFERENCE/DOCKET NUMBER: GI 5186A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 428 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-050-132A-2

Query Match 97.7%; Score 1336.5; DB 1; Length 428;
Best Local Similarity 98.4%; Pred. No. 5.2e-128;
Matches 253; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
QY 1 DVLDESETMDATGKTFELVSQDIRDEGWEETLEVSASVRRWRADSTTNKKNLEVTYOSH 60
| | | | |
Db 173 DVLDESETMDATGKTFELVSQDIRDEGWEETLEVSASVRRWRADSTTNKKNLEVTYOSH 232
QY 61 RESCOTLIDISVPSSKNLPFFVYVSNDRSNGTETRLDLKEMIGHBOETMLVKTAKNAY 120
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Db 233 RESCOTLIDISVPSSKNLPFFVYVSNDRSNGTETRLDLKEMIGHBOETMLVKTAKNAY 291

QY 121 OGAGESOESEGLDGYTAVGPLRLARRKSTGASSHCQTSIRVNFEDIGDMSWIIAPKEYD 180
| | | | |
Db 292 QVAGESOESEGLDGYTAVGPLRLARRKSTGASSHCQTSIRVNFEDIGDMSWIIAPKEYD 351
QY 181 AVECKGGEFFPLADVPPTKHAIVQTLVHLKFPYKGAACVPTKSPISILYKDDMGVP 240
| | | | |
Db 352 AVECKGGEFFPLADVPPTKHAIVQTLVHLKFPYKGAACVPTKSPISILYKDDMGVP 411
QY 241 TLKYHEGMSVAECGCR 257
| | | | |
Db 412 TLKYHEGMSVAECGCR 428

RESULT 3

US-08-750-222A-2
; Sequence 2, Application US/08750222A
; Patent No. 6034061
; GENERAL INFORMATION:
; APPLICANT: Wozney, Vicki A.
; APPLICANT: Celeste, Anthony J.
; APPLICANT: Song, Jeffrey
; APPLICANT: Thies, Scott
; TITLE OF INVENTION: BMP-9 COMPOSITIONS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: Legal Affairs - 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: US
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,222A
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/254,353
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kapinos, Ellen J.
; REGISTRATION NUMBER: 32,245
; REFERENCE/DOCKET NUMBER: GI 5186B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 428 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-750-222A-2

Query Match 97.7%; Score 1336.5; DB 3; Length 428;
Best Local Similarity 98.4%; Pred. No. 5.2e-128;
Matches 253; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
QY 1 DVLDESETMDATGKTFELVSQDIRDEGWEETLEVSASVRRWRADSTTNKKNLEVTYOSH 60
| | | | |
Db 173 DVLDESETMDATGKTFELVSQDIRDEGWEETLEVSASVRRWRADSTTNKKNLEVTYOSH 232
QY 61 RESCOTLIDISVPSSKNLPFFVYVSNDRSNGTETRLDLKEMIGHBOETMLVKTAKNAY 120
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Db 233 RESCOTLIDISVPSSKNLPFFVYVSNDRSNGTETRLDLKEMIGHBOETMLVKTAKNAY 291
QY 121 OGAGESOESEGLDGYTAVGPLRLARRKSTGASSHCQTSIRVNFEDIGDMSWIIAPKEYD 180
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Db 292 QVAGESEEEGLDGYTAAGPPLARRRSTGASHCQKTSLRVNFEDIGMDSWIAPREYD 351
OY 181 AYECGGCFPLADVTPTKHAIVOTLVHLKFPKVGACCVPTKLSPISTLYKDDMGVP 240
Db 352 AYECGGCFPLADVTPTKHAIVOTLVHLKFPKVGACCVPTKLSPISTLYKDDMGVP 411
OY 241 TLKYHEGMSVABCGCR 257
Db 412 TLKYHEGMSVABCGCR 428

RESULT 4
US-08-815-652B-2
Sequence 2, Application US/08815652B
Patent No. 6034062
GENERAL INFORMATION:
APPLICANT: Mooney, John M.
APPLICANT: Celeste, Anthony
APPLICANT: Song, Jeffrey
TITLE OF INVENTION: BMP-9 COMPOSITIONS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: Legal Affairs - 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: US
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,652B
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI 5186D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-815-652B-2

Query Match 97.7%; Score 1336.5; DB 3; Length 428;
Best Local Similarity 98.4%; Pred. No. 5.2e-128;
Matches 253; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

OY 1 DVLDESETWQATGCTKTFIVSODIRDEGWEETLEVSAYKRWVRADSTTNKKLEVTYQSH 60
Db 173 DVLDESETWQATGCTKTFIVSODIRDEGWEETLEVSAYKRWVRADSTTNKKLEVTYQSH 232
OY 61 RESCDTLDISVPPGSKNLPFFVFNDSRNGTKETRLDLKEMI GHEOTMLVYTAANAY 120
Db 233 RESCDTLDISVPPGSKNLPFFVFNDSRNGTKETRLDLKEMI GHEOTMLVYTAANAY 291
OY 121 QVAGESEEEGLDGYTAAGPPLARRRSTGASHCQKTSLRVNFEDIGMDSWIAPREYD 180
Db 292 QVAGESEEEGLDGYTAAGPPLARRRSTGASHCQKTSLRVNFEDIGMDSWIAPREYD 351
OY 181 AYECGGCFPLADVTPTKHAIVOTLVHLKFPKVGACCVPTKLSPISTLYKDDMGVP 240
Db 352 AYECGGCFPLADVTPTKHAIVOTLVHLKFPKVGACCVPTKLSPISTLYKDDMGVP 411

OY 241 TLKYHEGMSVABCGCR 257
Db 412 TLKYHEGMSVABCGCR 428

RESULT 5
US-08-254-353A-2
Sequence 2, Application US/08254353A
Patent No. 6287816
GENERAL INFORMATION:
APPLICANT: Rosen, Vicki A.
APPLICANT: Mooney, John M.
APPLICANT: Celeste, Anthony J.
APPLICANT: Song, Jeffrey
TITLE OF INVENTION: BMP-9 COMPOSITIONS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: Legal Affairs - 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: US
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/254,353A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI 5186B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-254-353A-2

Query Match 97.7%; Score 1336.5; DB 4; Length 428;
Best Local Similarity 98.4%; Pred. No. 5.2e-128;
Matches 253; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

OY 1 DVLDESETWQATGCTKTFIVSODIRDEGWEETLEVSAYKRWVRADSTTNKKLEVTYQSH 60
Db 173 DVLDESETWQATGCTKTFIVSODIRDEGWEETLEVSAYKRWVRADSTTNKKLEVTYQSH 232
OY 61 RESCDTLDISVPPGSKNLPFFVFNDSRNGTKETRLDLKEMI GHEOTMLVYTAANAY 120
Db 233 RESCDTLDISVPPGSKNLPFFVFNDSRNGTKETRLDLKEMI GHEOTMLVYTAANAY 291
OY 121 QVAGESEEEGLDGYTAAGPPLARRRSTGASHCQKTSLRVNFEDIGMDSWIAPREYD 180
Db 292 QVAGESEEEGLDGYTAAGPPLARRRSTGASHCQKTSLRVNFEDIGMDSWIAPREYD 351
OY 181 AYECGGCFPLADVTPTKHAIVOTLVHLKFPKVGACCVPTKLSPISTLYKDDMGVP 240
Db 352 AYECGGCFPLADVTPTKHAIVOTLVHLKFPKVGACCVPTKLSPISTLYKDDMGVP 411
OY 241 TLKYHEGMSVABCGCR 257
Db 412 TLKYHEGMSVABCGCR 428

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RESULT 6
PCT-US92-05374A-2
: Sequence 2, Application PC/TUS9205374A
: GENERAL INFORMATION:
: APPLICANT: Wozney, John M.
: APPLICANT: Celeste, Anthony
: TITLE OF INVENTION: BMP-9 COMPOSITIONS
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genetics Institute, Inc.
: STREET: Legal Affairs - 87 CambridgePark Drive
: CITY: Cambridge
: STATE: MA
: COUNTRY: US
: ZIP: 02140
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US92/05374A
: FILING DATE: 19920625
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Kapinos, Ellen J.
: REGISTRATION NUMBER: 32,245
: REFERENCE/DOCKET NUMBER: GI 5186A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 876-1170
: TELEFAX: (617) 876-5851
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 428 amino acids
: TYPE: AMINO ACID
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: PCT-US92-05374A-2

Query Match          97.7%; Score 1336.5; DB 5; Length 428;
Best Local Similarity 98.4%; Pred. No. 5,2e-128;
Matches 253; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 DVLDESEFMDOATGTTKTFLYSODIRDEGMETLEVSAYVKNRYRADSTNNKKLEVTYQSH 60
DB 173 DVLDESEFMDOATGTTKTFLYSODIRDEGMETLEVSAYVKNRYRADSTNNKKLEVTYQSH 232
QY 61 RESCDTLDISVPKSGKNLPFFVFSNDRSNGTKETRLDLKEMIGHDETMVYTKANAY 120
DB 233 RESCDTLDISVPKSGKNLPFFVFSNDRSNGTKETRLDLKEMIGHDETMVYTKANAY 291
QY 121 QGAGSDEEBEGLDGYTVAGPLARRKSTGASHCQKTSLRVNFEDIMDSMIAPKEYD 180
DB 292 QVAGESOEDEGLDGYTVAGPLARRKSTGASHCQKTSLRVNFEDIMDSMIAPKEYD 351
QY 181 AVECKGCGFFPLADVPTPKHAIVQTLVHLKPEPTKYGKACVPTKLSPISTLYKDDMGVP 240
DB 352 AVECKGCGFFPLADVPTPKHAIVQTLVHLKPEPTKYGKACVPTKLSPISTLYKDDMGVP 411
QY 241 TLKHYEGMSVAECGCR 257
DB 412 TLKHYEGMSVAECGCR 428

RESULT 7
PCT-US95-07084-2
: Sequence 2, Application PC/TUS9507084
: GENERAL INFORMATION:
: APPLICANT: Rosen, Vicki A.
: APPLICANT: Wozney, John M.
: APPLICANT: Celeste, Anthony J.
: TITLE OF INVENTION: BMP-9 COMPOSITIONS
: NUMBER OF SEQUENCES: 9
```

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: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genetics Institute, Inc.
: STREET: Legal Affairs - 87 CambridgePark Drive
: CITY: Cambridge
: STATE: MA
: COUNTRY: US
: ZIP: 02140
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/07084
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Kapinos, Ellen J.
: REGISTRATION NUMBER: 32,245
: REFERENCE/DOCKET NUMBER: GI 5186C-PCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 876-1210
: TELEFAX: (617) 876-5851
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 428 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: PCT-US95-07084-2

Query Match          97.7%; Score 1336.5; DB 5; Length 428;
Best Local Similarity 98.4%; Pred. No. 5,2e-128;
Matches 253; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 DVLDESEFMDOATGTTKTFLYSODIRDEGMETLEVSAYVKNRYRADSTNNKKLEVTYQSH 60
DB 173 DVLDESEFMDOATGTTKTFLYSODIRDEGMETLEVSAYVKNRYRADSTNNKKLEVTYQSH 232
QY 61 RESCDTLDISVPKSGKNLPFFVFSNDRSNGTKETRLDLKEMIGHDETMVYTKANAY 120
DB 233 RESCDTLDISVPKSGKNLPFFVFSNDRSNGTKETRLDLKEMIGHDETMVYTKANAY 291
QY 121 QGAGSDEEBEGLDGYTVAGPLARRKSTGASHCQKTSLRVNFEDIMDSMIAPKEYD 180
DB 292 QVAGESOEDEGLDGYTVAGPLARRKSTGASHCQKTSLRVNFEDIMDSMIAPKEYD 351
QY 181 AVECKGCGFFPLADVPTPKHAIVQTLVHLKPEPTKYGKACVPTKLSPISTLYKDDMGVP 240
DB 352 AVECKGCGFFPLADVPTPKHAIVQTLVHLKPEPTKYGKACVPTKLSPISTLYKDDMGVP 411
QY 241 TLKHYEGMSVAECGCR 257
DB 412 TLKHYEGMSVAECGCR 428

RESULT 8
US-08-065-844A-2
: Sequence 2, Application US/08065844A
: Patent No. 6333168
: GENERAL INFORMATION:
: APPLICANT: Tessell, Thomas M.
: APPLICANT: Basler, Konrad
: APPLICANT: Yomada, Toshiya
: TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF
: DORSALIN-1
: NUMBER OF SEQUENCES: 18
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Cooper & Dunham
: STREET: 30 Rockefeller Plaza
: CITY: New York
: STATE: New York
: COUNTRY: United States of America
```


ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/065,844A
FILING DATE: 19930520
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0516/40314
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 427 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-065-844A-2

Query Match 59.1%; Score 808.5; DB 4; Length 427;
Best Local Similarity 61.9%; Pred. No. 3.4e-74;
Matches 161; Conservative 31; Mismatches 59; Indels 9; Gaps 5;

QY 1 DVEDESETWQATGTFTFLVSODIRDEGWETLEVSAAVKRWVRADSTTNKKLEVTQSH 60
DB 174 DVL-DGDHWNKSTSLVSHSIDCGEMFEVSSAVKRWVKADKKTKKLEVTESK 232
QY 61 RES---CDTDISVPPGSKNIPFVFSNDRSNGTKERLDLKEHIGDEETLVYAK 117
DB 233 DLSGFPCKGKIDIVYHDTKNLPULVFSNDRSNGTKETKVE-LRMTVHEDESVLNKGK 291
QY 118 NAVGAGEGSEEBGLDGYAVGPLARRKSTGASSHCQKTSLRVNFEDIGDMSWIIAPK 177
DB 292 NDSSEEEQEEKAI--ARPROHSRSKRISGA-NHCRRISLHVNFREIGDMSWIIAPK 347
QY 178 EYDAYEKGCGCFPLADDTPTPKHAYQVTLKPTVAVGKACCVPTLSISILYKDDM 237
DB 348 DYENAEKGCGCFPLDNTVPTKHAIQVTLVHLNPKRASKACCVPTKLDIISTLYKDDA 407
QY 238 GVPTLKYEGMSVAEGCR 257
DB 408 GVPTLIYVYEGMKVAEGCR 427

RESULT 9
US-08-050-132A-9
Sequence 9, Application US/08050132A
Patent No. 5661007
GENERAL INFORMATION:
APPLICANT: Wozney, John M.
APPLICANT: Celeste, Anthony
TITLE OF INVENTION: BMP-9 COMPOSITIONS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: Legal Affairs - 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: US
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/050,132A
CLASSIFICATION: 435
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI 5186A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 150 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-050-132A-9

Query Match 46.3%; Score 634; DB 1; Length 150;
Best Local Similarity 92.7%; Pred. No. 4.3e-57;
Matches 114; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 135 YTAAGPLARRKSTGASSHCQKTSLRVNFEDIGDMSWIIAPKEYDAYECKGCGFPPLAD 194
DB 28 HVAAGSTLARRKRSAGASHCQKTSLRVNFEDIGDMSWIIAPKEYDAYECKGCGFPPLAD 87
QY 195 DVTPTKHAIVQTLVHLKPTPKVGVKACCVPTKISILYKDDMGVPTLKYHEGMSVAEC 254
DB 88 DVTPTKHAIVQTLVHLKPTPKVGVKACCVPTKISILYKDDMGVPTLKYHEGMSVAEC 147
QY 255 GCR 257
DB 148 GCR 150

RESULT 10
US-08-750-222A-9
Sequence 9, Application US/08750222A
Patent No. 6034061
GENERAL INFORMATION:
APPLICANT: Rosen, Vicki A.
APPLICANT: Wozney, John M.
APPLICANT: Celeste, Anthony J.
APPLICANT: Song, Jeffrey
TITLE OF INVENTION: BMP-9 COMPOSITIONS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: Legal Affairs - 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: US
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,222A
FILING DATE: 04-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/254,353
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI 5186B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 150 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-750-222A-9

Query Match 46.3%; Score 634; DB 3; Length 150;
Best Local Similarity 92.7%; Pred. No. 4.5e-57;
Matches 114; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 135 YTAAGPPLARRRSTGASSHCQKTSLRVNFEDIGWDSWIIAPKEYDAYECKGCGFFPLAD 194
DB 28 HVAAGSTLARRRSGAGSHCQKTSLRVNFEDIGWDSWIIAPKEYDAYECKGCGFFPLAD 87
QY 195 DVTPTKHAIVQTLVHLKPTKVGKACCVPTKLSPISTILYKDDMGVPTLKYHHEGMSVAEC 254
DB 88 DVTPTKHAIVQTLVHLKPTKVGKACCVPTKLSPISTILYKDDMGVPTLKYHHEGMSVAEC 147
QY 255 GCR 257
DB 148 GCR 150

RESULT 11

US-08-815-652B-9
Sequence 9, Application US/08815652B
Patent No. 6034062

GENERAL INFORMATION:
APPLICANT: Wozney, John M.
APPLICANT: Celeste, Anthony
APPLICANT: Song, Jeffrey
APPLICANT: Thies, R. Scott
TITLE OF INVENTION: BMP-9 COMPOSITIONS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.
STREET: Legal Affairs - 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: US
ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,652B

FILING DATE:

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:

NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI 5186D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 150 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-815-652B-9

Query Match 46.3%; Score 634; DB 3; Length 150;
Best Local Similarity 92.7%; Pred. No. 4.5e-57;
Matches 114; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 135 YTAAGPPLARRRSTGASSHCQKTSLRVNFEDIGWDSWIIAPKEYDAYECKGCGFFPLAD 194
DB 28 HVAAGSTLARRRSGAGSHCQKTSLRVNFEDIGWDSWIIAPKEYDAYECKGCGFFPLAD 87
QY 195 DVTPTKHAIVQTLVHLKPTKVGKACCVPTKLSPISTILYKDDMGVPTLKYHHEGMSVAEC 254
DB 88 DVTPTKHAIVQTLVHLKPTKVGKACCVPTKLSPISTILYKDDMGVPTLKYHHEGMSVAEC 147
QY 255 GCR 257
DB 148 GCR 150

DB 28 HVAAGSTLARRRSGAGSHCQKTSLRVNFEDIGWDSWIIAPKEYDAYECKGCGFFPLAD 87
QY 195 DVTPTKHAIVQTLVHLKPTKVGKACCVPTKLSPISTILYKDDMGVPTLKYHHEGMSVAEC 254
DB 88 DVTPTKHAIVQTLVHLKPTKVGKACCVPTKLSPISTILYKDDMGVPTLKYHHEGMSVAEC 147
QY 255 GCR 257
DB 148 GCR 150

RESULT 12

US-08-254-353A-9
Sequence 9, Application US/08254353A
Patent No. 6287816

GENERAL INFORMATION:
APPLICANT: Rosen, Vicki A.
APPLICANT: Wozney, John M.
APPLICANT: Celeste, Anthony J.
APPLICANT: Song, Jeffrey

APPLICANT: Thies, R. Scott
TITLE OF INVENTION: BMP-9 COMPOSITIONS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.
STREET: Legal Affairs - 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: US
ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/254,353A

FILING DATE:

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI 5186B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 150 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-254-353A-9

Query Match 46.3%; Score 634; DB 4; Length 150;
Best Local Similarity 92.7%; Pred. No. 4.5e-57;
Matches 114; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 135 YTAAGPPLARRRSTGASSHCQKTSLRVNFEDIGWDSWIIAPKEYDAYECKGCGFFPLAD 194
DB 28 HVAAGSTLARRRSGAGSHCQKTSLRVNFEDIGWDSWIIAPKEYDAYECKGCGFFPLAD 87
QY 195 DVTPTKHAIVQTLVHLKPTKVGKACCVPTKLSPISTILYKDDMGVPTLKYHHEGMSVAEC 254
DB 88 DVTPTKHAIVQTLVHLKPTKVGKACCVPTKLSPISTILYKDDMGVPTLKYHHEGMSVAEC 147
QY 255 GCR 257
DB 148 GCR 150

RESULT 13
PCT-US92-05374A-9

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Sequence 9, Application PC/TUS9205374A
GENERAL INFORMATION:
APPLICANT: Mooney, John M.
TITLE OF INVENTION: BMP-9 COMPOSITIONS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSER: Genetics Institute, Inc.
STREET: Legal Affairs - 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: US
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05374A
FILING DATE: 19920625
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI 5186A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 150 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US92-05374A-9

Query-Match
Best Local Similarity 92.7%; Pred. No. 4.5e-57;
Matches 114; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 135 YTAGPPLARRKRSSTGASHCOKTSLRVNFEDIGDMSWIAPEKDAYECKGCGFFPLAD 194
Db 28 HVAAGSTLARRKRSAGAGSHCOKTSLRVNFEDIGDMSWIAPEKEAEYCKGCGFFPLAD 87
QY 195 DVTPTKHAIVQTLVHLKFTPKVKGACCVPTKLSPTISILYKDDMGVPTLKYHEGMSVAEC 254
Db 88 DVTPTKHAIVQTLVHLKFTPKVKGACCVPTKLSPTISVLXKDDMGVPTLKYHEGMSVAEC 147
QY 255 GCR 257
Db 148 GCR 150

RESULT 14
PCT-US95-07084-9
Sequence 9, Application PC/TUS9507084
GENERAL INFORMATION:
APPLICANT: Rosen, Vicki A.
APPLICANT: Mooney, John M.
TITLE OF INVENTION: BMP-9 COMPOSITIONS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSER: Genetics Institute, Inc.
STREET: Legal Affairs - 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: US
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07084
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI 5186C-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1210
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 150 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-07084-9

Query-Match
Best Local Similarity 92.7%; Pred. No. 4.5e-57;
Matches 114; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 135 YTAGPPLARRKRSSTGASHCOKTSLRVNFEDIGDMSWIAPEKDAYECKGCGFFPLAD 194
Db 28 HVAAGSTLARRKRSAGAGSHCOKTSLRVNFEDIGDMSWIAPEKEAEYCKGCGFFPLAD 87
QY 195 DVTPTKHAIVQTLVHLKFTPKVKGACCVPTKLSPTISILYKDDMGVPTLKYHEGMSVAEC 254
Db 88 DVTPTKHAIVQTLVHLKFTPKVKGACCVPTKLSPTISVLXKDDMGVPTLKYHEGMSVAEC 147
QY 255 GCR 257
Db 148 GCR 150

RESULT 15
US-08-247-908A-2
Sequence 2, Application US/08247908A
Patent No. 5637480
GENERAL INFORMATION:
APPLICANT: CELESTE, Anthony J
APPLICANT: MOZNEY, John
TITLE OF INVENTION: BMP-10 COMPOSITIONS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSER: GENETICS INSTITUTE, INC.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02144
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/247,908A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: GI 5206-CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 876-1170 x8260
TELEFAX: 617 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 312 amino acids
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
us-08-247-908A-2

Query Match 38.0%; Score 519.5; DB 1; Length 312;
Best Local Similarity 42.8%; Pred. No. 6.1e-45;
Matches 119; Conservative 43; Mismatches 73; Indels 43; Gaps 10;

QY 1 DYLEPSTWDQATGKTFLVSODI--RDGEMTLEYSAYKRWVRADSTTNKRLLEVTVQ 58
DB 57 EYLESEKD-HGEGRNMVLVSGELVGNSEMETFDVTDALRHQKSGSST--HGLEVAHE 113
QY 59 SHRESCDT-----LDISVPPEGSKNLPFFVYFSNDRSNGTKETRLDLKEMIGHDEETMLV 113
DB 114 SKHEMEDTLGRGOLEIDTSAKNKHDPPLLVFSDDOJ--SEKERKELEDEMIHAHQ----- 166
QY 114 KTAKNAYOGAGEGSEEGLDGYTAVGP---LARRK-----RSTGASHCOKTS 159
DB 167 -----FPENDNDLDGYSN-GPGEHALLOMRSNIIYDSTARIRRNAGNYCKRTP 215
QY 160 LRVNFEIDIGMDSWIIAREYDAYECKGCGFFPLADYPTKHAIVQTLVHLKFTPKVGKA 219
DB 216 LYIDKEKIGMDSWIIAPPGEYAEYECRGVCNYPLEHLPKHAITQALVHLKNSQKASKA 275
QY 220 CCVPTKLSPIISILYKDDMGVPTLKYHGYGMSVAECGCR 257
DB 276 CCVPTKLEPISILYL-DKGVYTYKFKYEGMAVSECGCR 312

Search completed: April 2, 2003, 14:53:07
Job time: 30 secs

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: April 2, 2003, 14:46:20 ; Search time 86 Seconds
(without alignments)
615.745 Million cell updates/sec

Title: US-10-002-278-9
Perfect score: 1368
Sequence: 1 DVLEDSERWDQATGKTFLV.....GVPTLKYHEGMSVAECGR 257

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP:archaea:*
2: SP:bacteria:*
3: SP:fungi:*
4: SP:human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mhc:*
8: SP_organelle:*
9: SP_phage:*
10: SP_plant:*
11: SP_rodent:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*
15: SP_rvirts:*
16: SP_bacteriap:*
17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	357.5	26.1	411	5	09U418
2	352	25.7	361	5	096504
3	346	25.3	405	5	09U5E8
4	341	24.9	337	6	09WZV5
5	335.5	24.5	399	13	09W753
6	333	24.3	614	5	P91720
7	329.5	23.9	391	13	09W6C0
8	326.5	23.9	391	13	08UVG8
9	326.5	23.9	400	13	073818
10	326.5	23.9	400	13	091703
11	326.5	23.9	509	5	08W899
12	325.5	23.8	391	13	08UVQ2
13	325	23.8	588	5	09VQC6
14	320.5	23.4	438	5	09GCT26
15	320	23.4	391	13	090YJ3
16	319.5	23.4	400	13	090YD6

17	319.5	23.4	417	5	09XY07
18	319	23.3	254	5	09XZ69
19	319	23.3	257	13	042303
20	318	23.2	400	13	09PVK1
21	318	23.2	364	13	057574
22	316	23.1	411	13	057573
23	316	23.1	411	13	093369
24	315.5	23.1	412	13	012938
25	315	23.0	289	5	09XY08
26	314	23.0	398	13	090YD7
27	313	22.9	178	5	025211
28	311	22.7	400	13	013107
29	311	22.7	411	13	013108
30	310.5	22.7	277	13	090Y82
31	310.5	22.7	301	5	097390
32	310.5	22.7	313	13	091403
33	306	22.4	432	13	09PWF9
34	306	22.4	453	13	P87373
35	305	22.3	126	13	093573
36	304.5	22.3	500	13	09W6G0
37	302.5	22.1	398	13	091876
38	301.5	22.0	443	5	076851
39	300.5	22.0	390	13	091597
40	298.5	21.8	182	13	090Y81
41	298	21.8	424	13	09XG77
42	296	21.6	386	13	013109
43	294.5	21.5	294	6	09BDW9
44	294.5	21.5	497	6	09BDW8
45	293.5	21.5	413	13	09DGN4

ALIGNMENTS

RESULT 1	09U418	PRELIMINARY;	PRT;	411 AA.
ID	09U418			
AC	09U418;			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, last annotation update)			
DE	Bone morphogenetic protein 2/4.			
GN	BM2/4.			
OS	Branchiostoma belcheri (Amphioxus).			
OC	Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;			
OC	Branchiostoma.			
OX	NCBI_TaxID-7741;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Yasui K., Saiga H., Uemura M., Samba I.;			
RT	*Early body formation and expression pattern of genes encoding			
RT	secreted proteins, Bobmp2/4, Bwm17, and Bwm18 in lancelets.;			
RL	Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.			
CC	-i- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.			
DR	EMBL; AF206325; AAF19841.1; -			
DR	HSSP; P12643; 3BMP.			
DR	InterPro: IPR002405; Inhibin_alpha.			
DR	InterPro: IPR001839; TGFb.			
DR	InterPro: IPR001111; TGFb_N.			
DR	Pfam: PF00019; TGF-beta; 1.			
DR	Pfam: PF00688; TGFb_Propelide; 1.			
DR	PRINTS; PR00669; INHIBIN.			
DR	PRODOM; PD000357; TGFb; 1.			
DR	SMART; SM00204; TGFb; 1.			
DR	PROSITE; PS00250; TGF_BETA_1; 1.			
KW	Glycoprotein.			
SO	SEQUENCE 411 AA; 46929 MW; F579898060F18355 CRC64;			
Query Match	26.1%; Score 357.5; DB 5; Length 411;			
Best Local Similarity	35.5%; Pred. No. 2.2e-25;			
Matches	91; Conservative 29; Mismatches 87; Indels 49; Gaps 8;			
Oy	13 TGTFTPLVSG--DIRDEGWETLEVSAYKRWVRADSTTNKNKLEVTQVSHRESCDTLDI 69			

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DB 194 TDTITRLDITLVDRNSMESPVRSAVTKM--KNSPERNKYLEVEVVSFPRG----- 245
OY 70 SVPPSGKMLPEFVVSNDNRSGTKETRLDLKEMIGHDEETMLVTKAKNAYOGAESOE 129
DB 246 -----ALSNHVRRLRSTDMD--DHAMOHRRPLLTYYD---DGKSSMSN 286
OY 130 EGLDGYTAVGPELLARRKSTGASSH-----COKTSLRVNFEDIGWDSMTIAPREYDA 181
DB 287 R-----VASROKRAKGRKKHQRRLKANCRRHSLLYDFSDVGWMDMIVAPPGYQA 336
OY 182 YECGCGCEPPLADDTPTKHAIVQTLVHLKFPKVGKACCVPTKLSPISTILYKDDMGVPT 241
DB 337 YHCGECEPPLADHLNSTHNAIVQTLVNSVPLAVPACCVPTDLSPISTILYLNENDOVY 396
OY 242 LKRYEGMSVAECGCR 257
DB 397 LK-NYODMVEGCGCR 411
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RESULT 2

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096504 PRELIMINARY; PRT; 361 AA.
ID 096504
AC 096504;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Bone morphogenetic protein 2/4.
GN BMP2/4.
OS Brachyostoma floridae (Florida lancelet) (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OX NCBI_TaxID=7739;
RN [1]
RP MEDLINE=98401944; PubMed=9733108;
RX Paropoulos G.D., Clark M.D., Holland L.Z., Lehnach H., Holland N.D.;
RT "Amphioxus bone morphogenetic protein closely related
RT into evolution of dorsolateral axis specification."
RL Dev. Dyn. 213:130-139(1998).
CC -I SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL: AF068750; AAC97488.1; -.
DR HSSP: P12643; 3BMP.
DR InterPro: IPR002405; Inhibin_alpha.
DR InterPro: IPR001839; TGF-beta.
DR InterPro: IPR001111; TGF-beta.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGF-propeptide; 1.
DR PRINTS: PR00669; INHIBIN.
DR ProDom: PD000357; TGF-beta; 1.
DR SMART: SM00204; TGF-beta; 1.
DR PROSITE: PS00250; TGF-beta; 1.
KW Glycoprotein.
SQ SEQUENCE 361 AA; 41517 MW; 09FF5FE6C9789DD1 CRC64;
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Query Match 25.7%; Score 352; DB 5; Length 361;

Best Local Similarity 35.3%; Pred. No. 6e-25;

Matches 90; Conservative 31; Mismatches 86; Indels 48; Gaps 8;

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OY 13 TGTCTFLVSO---DIRDEGWTLEVSAYKRVADSTTNKKLEYTVQSHRESCDTLDT 69
DB 145 TDTITRLDITLVDRNSMESPVRSAVTKM--KNSPERNKYLEVEVVSFPRG----- 196
OY 70 SVPPSGKMLPEFVVSNDNRSGTKETRLDLKEMIGHDEETMLVTKAKNAYOGAESOE 129
DB 197 -----ALSNHVRRLRSTDMD--DHAMOHRRPLLTYYD---DGKSSMSN 237
OY 130 EGLDGYTAVGPELLARRKSTG-----ASHQOKTSLRVNFEDIGWDSMTIAPREYDA 182
DB 238 R-----VASROKRAKGRKKHQRRLKANCRRHSLLYDFSDVGWMDMIVAPPGYQA 287
OY 183 ECKGCGCEPPLADDTPTKHAIVQTLVHLKFPKVGKACCVPTKLSPISTILYKDDMGVPTL 242
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DB 288 YHCGECEPPLADHLNSTHNAIVQTLVNSVPLAVPACCVPTDLSPISTILYLNENDOVY 347
OY 243 KRYEGMSVAECGCR 257
DB 348 K-NYODMVEGCGCR 361
```

RESULT 3

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0905E8 PRELIMINARY; PRT; 405 AA.
ID 0905E8
AC 0905E8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE p4-BMP2/4.
GN p4-BMP2/4.
OS Ptychodera flava.
OC Eukaryota; Metazoa; Hemichordata; Enteropneusta; Ptychodoridae;
OC Ptychodera.
OX NCBI_TaxID=63121;
RN [1]
RP SEQUENCE FROM N.A.
RX Harada Y.;
RT Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX Okai N., Taguchi S., Tagawa K., Satoh N.;
RT "Developmental expression of hemichordate orthologs of BMP-4, otx and
RT dlx: Insights into deuterostome archetype and evolution of chordate
RT body plan."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -I SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL: AB028219; BAA89012.1; -.
DR HSSP: P12643; 3BMP.
DR InterPro: IPR002405; Inhibin_alpha.
DR InterPro: IPR001839; TGF-beta.
DR InterPro: IPR001111; TGF-beta.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGF-propeptide; 1.
DR PRINTS: PR00669; INHIBIN.
DR ProDom: PD000357; TGF-beta; 1.
DR SMART: SM00204; TGF-beta; 1.
DR PROSITE: PS00250; TGF-beta; 1.
KW Glycoprotein.
SQ SEQUENCE 405 AA; 45936 MW; D2EB2D2C7560ED13 CRC64;
```

Query Match 25.3%; Score 346; DB 5; Length 405;

Best Local Similarity 31.1%; Pred. No. 2.6e-24;

Matches 76; Conservative 43; Mismatches 71; Indels 54; Gaps 6;

```
OY 23 DIRDEGWTLEVSAYKRVADSTTNKKLEYTVQSHRESC---DTLDSVPP 73
DB 207 DIRNSMESPVRSAVTKM--KNSPERNKYLEVEVVSFPRG----- 266
OY 74 GSKNLPFEVVSNDNRSGTKETRLDLKEMIGHDEETMLVTKAKNAYOGAESOE 133
DB 267 WQROKRPRLTYYD---GKRPYR-----SKRNS----- 291
OY 134 GTTAVGPELLARRKSTGASSHCOKTSIRVNFEDIGWDSMTIAPREYDA 193
DB 292 -----ERKKGGRKLKPCRRSLYDFSDVGWMDMIVAPPGMAYICGCEPPLA 342
OY 194 DDTPTKHAIVQTLVHLKFPKVGKACCVPTKLSPISTILYKDDMGVPTLKYVEGMSVAE 253
DB 343 DHLNSTHNAIVQTLVHSKASAVPQACCVPTDLSPISTILYLDYDKVILK-NYODMVEG 401
OY 254 CGCR 257
DB 402 CGCR 405
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RESULT 4

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09MZV5
ID 09MZV5 PRELIMINARY: PRT: 337 AA.
AC 09MZV5:
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Bone morphogenetic protein 4 (Fragment).
GN BMP4.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
CX NCBI_TaxID=9615;
RN [1]
SEQUENCE FROM N.A.
RA Johnson J.A., Breen M., Lepine A., Murphy K.E.;
RT Identification and chromosomal localization of the gene encoding
RT canine bone morphogenetic protein 4 (bmp4).";
RL Submitted (MAR-1999) to the EMBL/Genbank/DDBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL: AF136233; AAF82188.1; -.
DR HSSP: P12643; 3BMP.
DR InterPro: IPR001839; TGFb_N.
DR InterPro: IPR001111; TGFb_N.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGFb_propeptide; 1.
DR ProDom: PD000357; TGFb; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF_BETA_1; 1.
KM Glycoprotein.
FT NON_TER
SQ SEQUENCE 337 AA; 38792 MW; BC91231431FPCA27 CRC64;

Query Match 24.9%; Score 341; DB 6; Length 337;
Best Local Similarity 35.4%; Pred. No. 6e-24;
Matches 84; Conservative 29; Mismatches 76; Indels 48; Gaps 7;

QY 29 WELEVSAAVKRWVRADSTTNKKLEVT---VQSHRSCTDIDISVPPGSKN---LPP 80
DB 141 WELEFVSPALVFWTRKOPRYGLAEVTHLHQTTHQCHVIRISKSLPQSGDMAQDRPL 200
QY 81 FVVFNSNDRNGTKETRLDLKEMIGHOEETMLVTKAKNAVAGAGSEEGEDGYAVGP 140
DB 201 LVTFGHD-GRGHALTRGRQAKRSRPHNAQR----- 229
QY 141 LLARKKSTASASHCQKTSIRVNFEDIGDMSIILPKKEYDAEKGCGCFPLADVPPTK 200
DB 230 --ARKK-----NKNCRSHSLYDFSDVGNMDIVAPRGVQAFYCHGDCPFLADHLNSTN 282
QY 201 HAIYQTLVHLKFPYKVGKACVPTKLSPIISILYKDDMGVPTLKYHEGMSVAECGCR 257
DB 283 HAIYQTLVNL-SVNSSIPKACCVPTLSAISMLYLDYKVKYLK-NYQDMVVEGCGCR 337

RESULT 5
ID 09W753 PRELIMINARY: PRT: 399 AA.
AC 09W753:
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Growth and differentiation factor 6.
GN GDF6.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodinae; Xenopus.
CX NCBI_TaxID=8355;
RN [1]
SEQUENCE FROM N.A.
RA MEDLINE-99396700; PubMed-10393114;
RA Chang C., Hemmati-Briylanlou A.;
RT "Xenopus GDF6, a new antagonist of noggin and a partner of BMPs.";
RL Development 126:3347-3357(1999).

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CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL: AF155125; AAD38402.1; -.
DR HSSP: P12643; 3BMP.
DR InterPro: IPR002405; Inhibin_alpha.
DR InterPro: IPR001839; TGFb_N.
DR InterPro: IPR001111; TGFb_N.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGFb_propeptide; 1.
DR PRINTS: PR00669; INHIBIN.
DR ProDom: PD000357; TGFb; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF_BETA_1; 1.
KM Glycoprotein.
SQ SEQUENCE 399 AA; 45571 MW; C549D973B50B8517 CRC64;

Query Match 24.5%; Score 335.5; DB 13; Length 399;
Best Local Similarity 34.2%; Pred. No. 2.5e-23;
Matches 89; Conservative 34; Mismatches 76; Indels 61; Gaps 11;

QY 23 DIRD---EGWETLEVSSAVKRWVRADSTTNKKLEVTYQSHRESCTDID-ISVPPGSKNL 78
DB 176 DIRTPSPGQVFPVY-----W-----KSLDIDISQKKQICVELKAISTLTGLE-- 218
QY 79 PFFVVFNSNDRNGTKETRLDLKEMIGHOEETMLV---TKAKNAVY-----CAGSEOE 128
DB 219 -----VNLS-----LGLARKPSHOEKALIVYFTKSSKKNLYNELKQVHSSKSME 265
QY 129 EEGLDGYTAVGPLARKRKSTGASSH-----CQKTSIRVNFEDIGDMSIILAPK 177
DB 266 KEARLHFKT-----RRRRRTFNRSRGRKGRKSRRLSCKPLHVFNEKELMDMIITAPL 320
QY 178 EYDAVECKGCGCFPLADVPPTKHAIVQTLVHLKFPYKVGKACVPTKLSPIISILYDDM 237
DB 321 EYEAHCEGCDPFLRSHLEPTNHALIOTLMSNMNRPSPSCCVPTKMTPTISILY-IDA 379
QY 238 GVPLTKHYBSMSVAECGCR 257
DB 380 GNNVYVRYQYEDMVVEGCGCR 399

RESULT 6
ID P91720 PRELIMINARY: PRT: 614 AA.
AC P91720:
DT 01-MAY-1997 (TREMblrel. 03, Created)
DT 01-MAY-1997 (TREMblrel. 03, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Decapentaplegic protein.
GN DPP.
OS Drosophila virilis (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
CX NCBI_TaxID=7244;
RN [1]
SEQUENCE FROM N.A.
RA MEDLINE-97225212; PubMed-9071585;
RA Newfield S.J., Padgett R.W., Findley S.D., Richter B.G., Sanicola M.,
RA de Cueva M., Gelbart W.M.;
RT "Molecular evolution at the decapentaplegic locus in Drosophila.";
RT Genetics 145:297-309(1997).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL: U63855; AAC47555.1; -.
DR HSSP: P12643; 3BMP.
DR FLYBase: FBgn0013109; Dv1r.dpp.
DR InterPro: IPR001839; TGFb_N.
DR InterPro: IPR001111; TGFb_N.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGFb_propeptide; 1.
DR ProDom: PD000357; TGFb; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF_BETA_1; 1.
KM Glycoprotein.

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SQ SEQUENCE 614 AA; 69055 MW; D0F20A4093403DCE CRC64;
Query Match 24.3%; Score 333; DB 5; Length 614;
Best Local Similarity 33.3%; Pred. No. 7.9e+23;
Matches 84; Conservative 37; Mismatches 87; Indels 44; Gaps 8;

OY 19 LVSDIDRDEGMEF--LEVSAVKRWVRADSTNKN-----KLEVTYQSHRESCD 65
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 394 LDTKTVRLNSTETVSLDVPADVRL---ATPOKNYGLLVEVRTMRSLPAPHHIVRLNR 450
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 66 TLUDISVPPGSKNLPEFVFNDSNGTKETRLDLKEMTGHDEQMLKTKAKNAQAGE 125
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 451 SADAEHEMOKKQPLFTTYTD---GHRKSR--SINDVSGR-----GGGNGGGR 496
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 126 SQEEGIDGYTAGVPLLRKSTGASSHCOKTSLRVNEDIGMDSWIIAREYDAVECK 185
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 497 NRRHQ-----RRSRKRNEDNCRHSLSLYVDQDGMSDMIAPPGYDAYCH 543
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 186 GGCFEPLADVDVPTKHAIVQTLVHLKFPTRKVGACGVPKLSILTKDDMGVPTLKX 245
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 544 GKCOEPLADHLNSTNHAVDTLVNMLNPGKVPKACCVPTQLEGISMLTNDORTVVLK-N 602
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 246 YEGMSVAECGR 257
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 603 YODMTVVGCGCR 614

RESULT 7
O9W6C0 PRELIMINARY; PRT; 261 AA.
AC 09W6C0: 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
GN Growth/differentiation factor 7 (Fragment).
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=99148135; Pubmed=10022976;
RA Davidson A.J., Postlethwait J.H., Yan Y.L., Belier D.R., van Doren C.,
RA Foenander D., Celeste A.J., Crosier K.E., Crosier P.S.;
RT "Isolation of zebrafish gdf7 and comparative genetic mapping of genes
RT belonging to the Growth/Differentiation factor 5, 6, 7 subgroup of the
RT TGF-beta superfamily."
RL Genome Res. 9:121-129(1999).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL: AF113023; AAD20829.1; -.
DR HSSP: P1643; JAMP
DR ZFIN: ZDB-GENE-990714-1; gdf7.
DR InterPro: IPR002400; GF_cyskn0t.
DR InterPro: IPR002405; Inhib1n_alpha.
DR InterPro: IPR001839; TGFb.
DR Pfam: PF00019; TGF-beta; 1.
DR PRINTS: PRO0438; GFCYSKN0T.
DR PRINTS: PRO0669; TNHINA.
DR ProDom: PD000357; TGFb. 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF_BETA_1; 1.
DR KMW Glycoprotein.
FT NON_TER 1
SQ SEQUENCE 261 AA; 29414 MW; 77346E977036A104 CRC64;

Query Match 24.1%; Score 329.5; DB 13; Length 261;
Best Local Similarity 31.6%; Pred. No. 5.1e+23;
Matches 84; Conservative 32; Mismatches 95; Indels 55; Gaps 7;

OY 23 DIRDEGMELEVSAAVKRWVRADSTNKN---LEVTVQSHRESCDITLIDISVPPGSKNL- 78
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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DB 20 DTSSATWDFDVGPILIKTPKQHTAEDTRLCLTSISAVS-----DSNNEAHPQMLGLS 74
OY 79 -----PEFVFNDSNGTKETRLDLKEMT-----GHEQETM 111
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 75 REDQOTERRALLVAFSQAR---RKENLFREIRKLIAMSKRFSPNTEPHSKGPRNR 131
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 112 LVKTAKNAYQAGAGESQEEGIDGYTAGVPLLRKSTGASSHCOKTSLRVNEDIGMS 171
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 132 RRRRA-----LAGRPYGPIITSGCGRRRTCSRKPLHVFKELGWMD 176
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 172 WIIAREYDAVECKGGCFEPLADVDVPTKHAIVQTLVHLKFPTRKVGACGVPKLSPI 231
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 177 WIIAREYDAVECKGGCFEPLADVDVPTKHAIVQTLVHLKFPTRKVGACGVPKLSPI 236
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 232 LYKDDMGVPTLKXHYEGMSVAECGR 257
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 237 LYIDS-GNNVYKQYEDMVAESGCR 261

RESULT 8
O8UV08 PRELIMINARY; PRT; 391 AA.
AC O8UV08: 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Anti-dorsalizing morphogenetic protein.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=21614694; Pubmed=11748836;
RA Lele Z., Nowak M., Hubmerschmidt M.;
RT "zebrafish damp is required to restrict the size of the organizer and
RT to promote posterior and ventral development.";
RL Dev. Dyn. 222:681-687(2001).
DR EMBL: AF418564; AAL49502.1; -.
DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001111; TGFb_N.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGFb_propeptide; 1.
DR ProDom: PD000357; TGFb. 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF_BETA_1; UNKNOWN.1.
DR PROSITE: PS00250; TGF_BETA_1; 1.
SQ SEQUENCE 391 AA; 43792 MW; F89885D22364962B CRC64;

Query Match 23.9%; Score 326.5; DB 13; Length 391;
Best Local Similarity 32.3%; Pred. No. 1.7e+22;
Matches 87; Conservative 43; Mismatches 92; Indels 47; Gaps 11;

OY 5 DSEWDAQTKTFLVSO---DIRDEGMELEVSAAVKRWVRADSTNKNKLEVTYQSHR 61
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 154 DSKKNVYQGRK--LLSSRLVPIHSTGMEVFTTQAVRSM--SDGSGNIGLL-VSVRLA 209
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 62 ESCDITLIDISVPPGSKNLPEFVFNDSNGTKETRLDLKEMTGHDEQMLKTKAKNAYQ 121
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 210 GS-QMDLKM-----VRFASGDH-----HNSKQMLVLFPTDQRR 243
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 122 GAGESQEEGID---GYTAGVPLLRKST-----GASSHCOKTSLRVNEDIGM 169
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 244 AASLEATSKGSDVSPGXSQLPVPVPSRRSSVDYDERGKRMACQROPLVYVDEEELG 303
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 170 DSMIIAREYDAVECKGGCFEPLADVDVPTKHAIVQTLVH-LKFPTRKVGACGVPKLS 228
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 304 SGWIVSPGYMAHYCKSCIFPLSQNNRPTNHAIYQSLINTLKLKNGIQTFPCVDPKLYS 363
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 229 ISILKDDMGVPTLKXHYEGMSVAECGR 257
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 364 ISLAFYDDDENYVLK-QYDDMVAESGCR 391
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 9
073818 PRELIMINARY; PRT; 400 AA.
AC 073818;
DT 01-AUG-1998 (TREMblrel. 07, Created)
DT 01-AUG-1998 (TREMblrel. 07, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Bone morphogenetic protein 4.
GN BMP-4.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP MEDLINE=98440832; PubMed=9753664;
RA Kim J., Ault K.T., Chen H.D., Xu R.H., Roh D.H., Lin M.C., Park M.J.,
RA Kung H.F.;
RT "Transcriptional regulation of BMP-4 in the Xenopus embryo: analysis
RT of genomic BMP-4 and its promoter.";
RL Biochem. Biophys. Res. Commun. 250:516-530(1998).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL: AF058764; AAC61694.1; -.
DR HSSP: P12643; 3BMP.
DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001111; TGFb_N.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGF-propeptide; 1.
DR ProDom: PD000357; TGFb; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF_BETA_1; 1.
KW Glycoprotein.
SQ
SEQUENCE 400 AA; 45810 MW; A3147EAFACBA553F CRC64;

Query Match 23.9%; Score 326.5; DB 13; Length 400;
Best Local Similarity 32.8%; Pred. No. 1.8e-22;
Matches 78; Conservative 35; Mismatches 72; Indels 53; Gaps 7;

OY 29 WETLEVSAAKRVNRADSTNNKRLKLEV-----TVQSHRSCDTLDSVPP-----GSKNLP 79
DB 207 WESFDVSPALMRRTRKQINHGALIEFVILNQTCKHQKHRISSLLPQEDAMWSQMRP 266
OY 80 FFFVFSNDNSNGKTRRLDLKEMIGHQETMLVKTANNAYQAGASEOEERGLDGYTAVG 139
DB 267 LLITFSHDGR-----GH-----ALTRRSKRS----- 287
OY 140 PLARRRSTGASGHSCKTSLRVNFEIDIGMSIITAPKEYDAYECKGCEPPLADVTPT 199
DB 288 ---PKQORPPKKKKHCKRRSLVYDFSDVGNNMVIYAPGYQAFYCHGDCPPPLADHINST 344
OY 200 KHAIVQTLVHLKFPYVGAACVPTKLSPISTILYKDDMGVPTLKRYHFGMSVAECGR 257
DB 345 NHAIVQTLVN-SYNASIPKACVPTKLSPISTILYKDDMGVPTLKRYHFGMSVAECGR 400

RESULT 10
091703 PRELIMINARY; PRT; 400 AA.
AC 091703;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Protein 4.
GN BMP-4.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.

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RA Smith J.C.;
RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-20 FROM N.A.
RX MEDLINE=93048819; PubMed=1425340;
RA Dale L., Howes G., Price B.M., Smith J.C.;
RT "Bone morphogenetic protein 4: a ventralizing factor in early Xenopus
RT development.";
RL Development 115:573-585(1992).
RN [3]
RP SEQUENCE FROM N.A.
RA Metz A., Knoechel S., Buechler P., Koester M., Knoechel W.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL: X64538; CAA45836.1; -.
DR EMBL: A1005076; CAA06333.1; -.
DR HSSP: P12643; 3BMP.
DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001111; TGFb_N.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGF-propeptide; 1.
DR ProDom: PD000357; TGFb; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF_BETA_1; 1.
KW Glycoprotein.
SQ
SEQUENCE 400 AA; 45778 MW; B81472F9BCBA506E CRC64;

Query Match 23.9%; Score 326.5; DB 13; Length 400;
Best Local Similarity 32.8%; Pred. No. 1.8e-22;
Matches 78; Conservative 35; Mismatches 72; Indels 53; Gaps 7;

OY 29 WETLEVSAAKRVNRADSTNNKRLKLEV-----TVQSHRSCDTLDSVPP-----GSKNLP 79
DB 207 WESFDVSPALMRRTRKQINHGALIEFVILNQTCKHQKHRISSLLPQEDAMWSQMRP 266
OY 80 FFFVFSNDNSNGKTRRLDLKEMIGHQETMLVKTANNAYQAGASEOEERGLDGYTAVG 139
DB 267 LLITFSHDGR-----GH-----ALTRRSKRS----- 287
OY 140 PLARRRSTGASGHSCKTSLRVNFEIDIGMSIITAPKEYDAYECKGCEPPLADVTPT 199
DB 288 ---PKQORPPKKKKHCKRRSLVYDFSDVGNNMVIYAPGYQAFYCHGDCPPPLADHINST 344
OY 200 KHAIVQTLVHLKFPYVGAACVPTKLSPISTILYKDDMGVPTLKRYHFGMSVAECGR 257
DB 345 NHAIVQTLVN-SYNASIPKACVPTKLSPISTILYKDDMGVPTLKRYHFGMSVAECGR 400

RESULT 11
08WS99 PRELIMINARY; PRT; 509 AA.
AC 08WS99;
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Bone morphogenetic protein BMP2/4.
OS Archaster typicus.
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
OC Asteroidea; Valvatacea; Valvatida; Archasteridae; Archaster.
OX NCBI_TaxID=136937;
RN [1]
RP SEQUENCE FROM N.A.
RA Shih L.-J., Chen C.-P., Hwang S.-P.L.;
RT "Uniform Distribution of Sea Star BMP2/4 mRNA in Embryos at the Later
RT Stages of Embryonic Development.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF334705; AAL73188.1; -.
DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001111; TGFb_N.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGF-propeptide; 1.
DR ProDom: PD000357; TGFb; 1.
DR SMART: SM00204; TGFb; 1.

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DR InterPro: IPR001111; TGFb_N.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGFb_propeptide; 1.
DR PRINTS: PR00669; INHIBINA.
DR ProDom: PD000357; TGFb; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF_BETA_1; 1.
KW Glycoprotein.
SQ
SEQUENCE 588 AA; 65867 MW; 2C8166C1BD2F666B CRC64;

Query Match          23.8%; Score 325; DB 5; Length 588;
Best Local Similarity 30.5%; Pred. No. 4,2e-22;
Matches 92; Conservative 46; Mismatches 114; Indels 50; Gaps 9;

OY 4 EDEETWDATGTTFLVSODIR---DEGMETLEY---SSAVKVRADSTNNKKLEY 55
DB 289 KDSKIDRRPHNNHFRHNDVKSIPADEKLAELQLTROLSCQVYASSANRRIRYOV 348
OY 56 T-----VQSHRE-----SCDTLDISVPG-----SKNLPFYVES 85
DB 349 LVYDITRVGVRGQREPSYLLDPTKTVRLNSTDTVSIDVQPAVDMLASPORNYGLLVEVR 408
OY 86 NDSS-----NCTKERTLDLKEMIGHOEETMLVTKAKNAVQAGASQOEELDGYTAV 138
DB 409 TVSLKRPAPRNHNYRLRSADHAEHWMQKQRLPFTYTDGGRK-ARSTRVYSGEGGGGK 467
OY 139 GPLLARKKSTGASH---CQKTSLRVNEFDIGWDSWIIAPKEYDAEKGCGCFPLADD 195
DB 468 GRNKRQPRRRRTKRKHNDDICRRHSILYDFSDGMDMDIVAPLGDATYCGKGFPLADH 527
OY 196 VTPKHAIVQTLVHLKFTPKVGKACVPKTLSPISILYKDDMGVPTLKYHVEGSAVECG 255
DB 528 FNSNNAHVQGLTVLNMNPKVKPACCPVGLDVSAMLYLNDQSTVVLK-NYQENTVYVCG 586
OY 256 CR 257
DB 587 CR 588

RESULT 14
O9GT26 PRELIMINARY; PRT: 438 AA.
ID O9GT26;
AC O9GT26;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Gb-60a-like protein As60a.
OS Anopheles stephensi (Indo-Pakistan malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
OC Anopheles.
OX NCBI_TaxID=30069;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2106562; PubMed=11145845;
RA Crampston A.L., Luckhart S.;
RT "Isolation and characterization of As60a, a transforming growth
RT factor-beta gene, from the malaria vector Anopheles stephensi.";
RL Cytokine 13,65-74(2001).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL: AF284816; AAC13400.1; -.
DR HSSP: P18075; IBMF.
DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001111; TGFb_N.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGFb_propeptide; 1.
DR ProDom: PD000357; TGFb; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF_BETA_1; 1.
KW Glycoprotein.
SQ
SEQUENCE 438 AA; 49824 MW; 124BA66DA832E84 CRC64;

Query Match          23.4%; Score 320.5; DB 5; Length 438;

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Best Local Similarity 30.4%; Pred. No. 7,5e-22;
Matches 82; Conservative 21; Mismatches 70; Indels 97; Gaps 6;

OY 27 EGMETLEVSASVRWVR-----ADSTNNKLETVQSHRECDPLDISVP 72
DB 225 EGMELIVTAVLMLKNNQAHGLYIGAFEDRYERVKLD-----DIGVSAAR 274
OY 73 PGSKNLPFYVESNDKSNCTKTRIDLKEMIGHOEETMLVTKAKNAVQAGASQOEEL 132
DB 275 GSDEYQPELVVANSOQOMK----- 295
OY 133 DGYTAVGPLAR-----RRKSTGASH-----CQKTSLRVNEFD 166
DB 296 -----PILORLHLTRNKRSPSRKRKPKTEHHPQYHOPYDOHKSCRIOOLYVSFKD 348
OY 167 IGDWSWIIAPKEYDAEKGCGCFPLADYPTKALVQTLVHLKFTPKYKACVPKTL 226
DB 349 LQHWEMWIIAPKEYGAYVCGEGCPFLAHMNTATVOTLHNPFTKVPKPCAPTKL 408
OY 227 SPISILYKDDMGVPTLKYHVEGSAVECG 256
DB 409 IPISTLYHIDEANVNLK-KYKNMVVSCGC 437

RESULT 15
O90YJ3 PRELIMINARY; PRT: 391 AA.
ID O90YJ3;
AC O90YJ3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Anti-dorsalizing morphogenetic protein.
OS ADMP.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Peyrieras N.;
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Willott V.;
RT "Cooperative action of ADMP and BMP mediated pathways in regulating
RT cell fates in the zebrafish gastrula.";
RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL: AJ315468; CAC50881.1; -.
DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001111; TGFb_N.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGFb_propeptide; 1.
DR ProDom: PD000357; TGFb; 1.
DR PROSITE: PS00250; TGF_BETA_1; UNKNOWN_1.
KW Glycoprotein.
SQ
SEQUENCE 391 AA; 43789 MW; 69CC73A98702BBD7 CRC64;

Query Match          23.4%; Score 320; DB 13; Length 391;
Best Local Similarity 32.9%; Pred. No. 7,1e-22;
Matches 82; Conservative 37; Mismatches 84; Indels 46; Gaps 10;

OY 24 IRDGMETLEVSASVRWVRADSTNNKLETVQSHRECDPLDISVPKSKNLPFYV 83
DB 174 IHSTGMEVFTITQAVRSWM-SDGSLGLL-VSVRTLAGS-QQDLKM-----VR 219
OY 84 FSNDRSKTETRLDLKEMIGHOEETMLVTKAKNAVQAGASQOEELDGYTAVG---- 139
DB 220 FASGRDH-----HNSKQPMVLVLTPTDGRRAASLEATSKGSD--VSPGSPQ 263
OY 140 -----PLARRKST-----GASSHCQKTSLRVNEFDIGWDSWIIAPKEYDAEKGCGCF 189

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Db 264 PLPSVPASRRSPRSVDYDERGEMACORPLVYDFEEIGWSGIVSPKGYNAHCKGSCI 323
 QY 196 PPLADDDVPTPKHAIYOTLVH-LKFPPTKVGKACCVPTKLSPLSYKDDMGVPTLKHYHEG 248
 Db 324 PPLSONMRPTNHAIYOSIINTLKNKGIOPTCCVDPDKLYSISLHFDDEENVYLK-QYTD 382
 QY 249 MSVAECGCR 257
 Db 383 MVAGSGCGR 391

Search completed: April 2, 2003, 14:51:41
 Job time : 88 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 2, 2003, 14:40:40 ; Search time 26 Seconds
(without alignments)
409.978 Million cell updates/sec

Title: US-10-002-278-9

Perfect score: 1368
Sequence: 1 DVLDESETMDQATGTKTFLV.....GVPTLKHYEGMSVAECGR 257

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1349.5	98.6	428	1	GDF2_MOUSE
2	1146.5	83.8	429	1	GDF2_HUMAN
3	808.5	59.1	427	1	DSL1_CHICK
4	516.5	37.8	424	1	BMP10_HUMAN
5	507	37.1	420	1	BMP10_MOUSE
6	345	25.2	408	1	BMP4_HUMAN
7	342.5	25.0	408	1	BMP4_MOUSE
8	341	24.9	408	1	BMP4_DANDA
9	337.5	24.7	408	1	BMP4_MOUSE
10	336	24.6	409	1	BMP4_RABIT
11	330	24.1	436	1	GDF6_BOVIN
12	327.5	23.9	405	1	BMP4_CHICK
13	325	23.8	588	1	DECA_DROME
14	324.5	23.7	621	1	DECA_DROSI
15	323	23.6	593	1	DECA_DROSI
16	319	23.3	398	1	BMP8_XENLA
17	316.5	23.1	401	1	BMP8_XENLA
18	316	23.1	395	1	BMP2_RABIT
19	315	23.0	398	1	BMP2_RABIT
20	314.5	23.0	430	1	BMP8_XENLA
21	314	23.0	393	1	BMP2_MOUSE
22	313	22.9	394	1	BMP2_MOUSE
23	312.5	22.8	454	1	BMP5_HUMAN
24	312	22.8	125	1	GDF6_MOUSE
25	311	22.7	396	1	BMP2_HUMAN
26	311	22.7	399	1	BMP8_MOUSE
27	310.5	22.7	461	1	DVRL_STRPU
28	310	22.7	396	1	BMP2_DANDA
29	307	22.4	353	1	BMP2_CHICK
30	305.5	22.4	501	1	GDF5_HUMAN
31	305.5	22.3	431	1	BMP7_HUMAN
32	305.5	22.3	452	1	BMP5_MOUSE
33	305.5	22.3	495	1	GDF5_MOUSE

34	301	22.0	402	1	BMP8_HUMAN	P34820	homo sapien
35	301	22.0	510	1	BMP6_MOUSE	P20722	mus musculus
36	298	21.8	513	1	BMP6_HUMAN	P22004	homo sapien
37	297	21.7	426	1	BMP7_XENLA	P30886	xenopus lae
38	294.5	21.5	436	1	60A_DROVI	Q24735	drosophila
39	294	21.5	151	1	GDF7_MOUSE	P43029	mus musculus
40	290	21.2	360	1	DVRL_XENLA	P09534	xenopus lae
41	289.5	21.2	355	1	DVRL_BRARE	P35621	brachydanio
42	285	20.8	354	1	NODA_MOUSE	P43021	mus musculus
43	281	20.5	207	1	BMP6_RAT	Q04806	rattus norv
44	276.5	20.2	372	1	DECA_FRIKA	Q26574	tritidolum c
45	274.5	20.1	455	1	60A_DROME	P27091	drosophila

ALIGNMENTS

RESULT 1
GDF2_MOUSE STANDARD; PRT; 428 AA.
AC Q9WV56; Q9Q2E0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Growth/differentiation factor 2 precursor (GDF-2) (Bone morphogenetic protein 9) (BMP-9).
GN GDF2 OR BMP9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN-CD-1; TISSUE=Liver;
RA Zimmers T.A., Konlaris L.G., Sitzmann J.V., Lee S.-J.;
RT "Growth/differentiation factor-2, a new TGF-beta family member with bone promoting activities";
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Celeste A.J.;
RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.
CC -!- FUNCTION: COULD BE INVOLVED IN BONE FORMATION.
CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC -----
CC EMBL: ARI56890; AAD40308.1; -;
CC EMBL: ARI80286; AAD56961.1; -;
CC HISP; P12643; 3BMP.
CC MGD; MG1:1321394; Gdf2.
CC InterPro: IPR002405; Inhibin_alpha.
CC InterPro: IPR001839; TGFb.
CC InterPro: IPR001111; TGFb_N.
CC Pfam: PF00019; TGF-beta; 1.
CC Pfam: PF00688; TGFb_propeptide; 1.
CC PRINTS: PRO0066; INHIBINA.
CC PRODom: PD000357; TGFb; 1.
CC SMART: SM00204; TGFb; 1.
CC PROSITE: PS00250; TGF-BETA_1; 1.
CC SIGNAL: Growth factor; Cytokine; Glycoprotein.
CC FT SIGNAL: 1 22 POTENTIAL.
CC FT PROPEP 23 318 BY SIMILARITY.
CC CHAIN 319 428 GROWTH/DIFFERENTIATION FACTOR 2.

FT DISULFID 326 392 BY SIMILARITY.
 FT DISULFID 355 425 BY SIMILARITY.
 FT DISULFID 359 427 BY SIMILARITY.
 FT DISULFID 391 391 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 293 293 G -> V (IN REF. 2).
 FT CONFLICT 382 382 K -> E (IN REF. 2).
 SQ SEQUENCE 428 AA; 47660 MW; 6B81525FF8A76A39 CRC64;

Query Match 98.6%; Score 1349.5; DB 1; Length 428;
 Best Local Similarity 99.2%; Pred. No. 1.1e-112;
 Matches 253; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 DYLEDSEETWDATGKTFTFLVSODIRDEGMETLEVSAAVRWYRADSTTNKKLEVTYQSH 60
 DB 173 DYLEDSEETWDATGKTFTFLVSODIRDEGMETLEVSAAVRWYRADSTTNKKLEVTYQSH 232

QY 61 RESCDTLDISVPSSKNLPFFVVSNDRSNGTKETRLDLMKMGHEDETMVYTKAKAY 120
 DB 233 RESCDTLDISVPSSKNLPFFVVSNDRSNGTKETRLDLMKMGHEDETMVYTKAKAY 291

QY 121 OGAGSDEEGLDGYAVGPLARRRKSTGASSHCCKTSLRVNFEDIGMDSMTIAPKEYD 180
 DB 292 OGAGSDEEGLDGYAVGPLARRRKSTGASSHCCKTSLRVNFEDIGMDSMTIAPKEYD 351

QY 181 AYECKGCFPLADVTPTKHAIVOTLVHLKPTKYGKACVPTLSPISILYKDDMGVP 240
 DB 352 AYECKGCFPLADVTPTKHAIVOTLVHLKPTKYGKACVPTLSPISILYKDDMGVP 411

QY 241 TLKYHYEGMSVAECGR 257
 DB 412 TLKYHYEGMSVAECGR 428

RESULT 2
 GDF2_HUMAN STANDARD; PRT; 429 AA.
 ID GDF2_HUMAN
 AC 09UK05; Q9Y571;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Growth/differentiation factor 2 precursor (GDF-2) (Bone morphogenetic protein 9) (BMP-9).
 GN GDF2 OR BMP9.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Celeste A.J.;
 RU Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 316-429 FROM N.A.
 RC TISSUE=Liver;
 RA Zimmer's L.A.; Koniaris L.G.; Sltzmann J.V.; Lee S.-J.;
 RT "Growth/differentiation factor-2, a new TGF-beta family member with bone promoting activities."
 RU Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: COULD BE INVOLVED IN BONE FORMATION.
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC -----
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CC or send an email to license@isb-sib.ch.
 CC EMBL; AF186285; AAD56960.1; -;
 DR EMBL; AF186891; AAD40309.1; -;
 DR HSSE; P18075; IBMP.
 DR Genew; HGNC:4217; GDF2.
 DR MIM; 605120; -;
 DR Interpro; IPR002405; Inhbln_alpha.
 DR Interpro; IPR001839; TGFp.N.
 DR Interpro; IPR001111; TGFp.N.
 DR Pfam; PF000019; TGF-beta; 1.
 DR Pfam; PF00688; TGFp-propeptide; 1.
 DR PRINTS; PR00669; INHIBIN.
 DR PRODOM; PD000357; TGFp; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Signal; Growth factor; Cytokine; Glycoprotein.
 FT SIGNAL 1 22
 FT PROPEP 23 319
 FT CHAIN 320 429
 FT DISULFID 327 393
 FT DISULFID 356 426
 FT DISULFID 360 428
 FT DISULFID 392 392
 FT CARBOHYD 71 71
 FT CARBOHYD 136 136
 SQ SEQUENCE 429 AA; 47320 MW; 5AC15DCA205FF086 CRC64;

Query Match 83.8%; Score 1146.5; DB 1; Length 429;
 Best Local Similarity 82.9%; Pred. No. 1.3e-94;
 Matches 213; Conservative 19; Mismatches 24; Indels 1; Gaps 1;

QY 1 DYLEDSEETWDATGKTFTFLVSODIRDEGMETLEVSAAVRWYRADSTTNKKLEVTYQSH 60
 DB 174 DYLEDSEETWDATGKTFTFLVSODIRDEGMETLEVSAAVRWYRADSTTNKKLEVTYQSH 233

QY 61 RESCDTLDISVPSSKNLPFFVVSNDRSNGTKETRLDLMKMGHEDETMVYTKAKAY 120
 DB 234 RESCDTLDISVPSSKNLPFFVVSNDRSNGTKETRLDLMKMGHEDETMVYTKAKAY 292

QY 121 OGAGSDEEGLDGYAVGPLARRRKSTGASSHCCKTSLRVNFEDIGMDSMTIAPKEYD 180
 DB 293 OGAGSDEEGLDGYAVGPLARRRKSTGASSHCCKTSLRVNFEDIGMDSMTIAPKEYD 352

QY 181 AYECKGCFPLADVTPTKHAIVOTLVHLKPTKYGKACVPTLSPISILYKDDMGVP 240
 DB 353 AYECKGCFPLADVTPTKHAIVOTLVHLKPTKYGKACVPTLSPISILYKDDMGVP 412

QY 241 TLKYHYEGMSVAECGR 257
 DB 413 TLKYHYEGMSVAECGR 429

RESULT 3
 DSL1_CHICK STANDARD; PRT; 427 AA.
 ID DSL1_CHICK
 AC P34822;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Dorsalin-1 precursor (DSL-1).
 GN DSL-1.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.; AND SEQUENCE OF 319-322.
 RC TISSUE=Spinal cord;
 RX MEDLINE-93272310; PubMed-7916656;
 RA Bailer K., Edlund T., Jessell T.M., Yamada T.;
 RT "Control of cell pattern in the neural tube: regulation of cell

```

RT differentiation by dorsalin-1, a novel TGF beta family member."
CC Cell 73:687-702(1993).
CC
CC -1- FUNCTION: APPEARS TO REGULATE CELL DIFFERENTIATION WITHIN THE
CC NEURAL TUBE. MAY REGULATE THE DIFFERENTIATION OF CELL TYPES ALONG
CC THE DORSOVENTRAL AXIS OF THE NEURAL TUBE, ACTING IN CONJUNCTION
CC WITH DISTINCT VENTRALIZING SIGNALS FROM THE NOTOCHORD AND FLOOR
CC PLATE. CONTROLS THE CELL DIFFERENTIATION IN THE NEURAL TUBE IN
CC SEVERAL WAYS: (1) PROMOTES THE DIFFERENTIATION OF CELL TYPES THAT
CC DERIVE FROM THE DORSAL NEURAL TUBE. (2) ENSURES THAT THE DORSAL
CC NEURAL TUBE IS REFRACTORY TO VENTRALIZING SPECIES FROM THE
CC NOTOCHORD. (3) CAN DEFUSE AND INFLUENCE THE FATE OF CELLS IN MORE
CC VENTRAL REGIONS OF THE NEURAL TUBE.
CC
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
CC
CC -1- SUBCELLULAR LOCATION: Secreted.
CC
CC -1- TISSUE SPECIFICITY: EXPRESSED SELECTIVELY IN THE DORSAL NEURAL
CC TUBE. LOWER LEVELS SEEN IN KIDNEY AND MYOTOMAL CELLS.
CC
CC -1- DEVELOPMENTAL STAGE: IS NOT EXPRESSED IN NEURAL CELLS AT STAGES
CC BEFORE NEURAL TUBE CLOSURE. IS EXPRESSED AT HIGH LEVELS IN THE
CC DORSAL THIRD OF THE NEURAL TUBE, BEGINNING AT THE TIME OF NEURAL
CC TUBE CLOSURE, BUT NOT BY VENTRAL NEURAL CELLS OR BY NONNEURAL
CC CELLS. DORSAL RESTRICTION PERSISTS IN THE SPINAL CORD AT STAGES
CC AFTER THE ONSET OF NEURONAL DIFFERENTIATION. AT LATER STAGES OF
CC SPINAL DEVELOPMENT, IS RESTRICTED TO THE DORSOMEDIAL REGION OF
CC THE SPINAL CORD, INCLUDING BUT NOT CONFINED TO THE ROOF PLATE.
CC
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
CC -----
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CC
CC
CC EMBL: L12032; AAA48752.1; -.
CC PIR: A40735; A40735.
CC
CC HSSP: P12643; 3BMP.
CC
CC InterPro: IPR001839; TGFb.
CC
CC InterPro: IPR001111; TGFb_N.
CC
CC Pfam: PF000019; TGF-beta; 1.
CC
CC Pfam: PF00688; TGFb_propeptide; 1.
CC
CC ProDom: PD000357; TGFb; 1.
CC
CC SMART: SM00204; TGFb; 1.
CC
CC PROSITE: PS00250; TGF_BETA_1; 1.
CC
CC Signal: Growth factor; Cytokine; Glycoprotein.
CC
CC FT SIGNAL 1 20
CC FT PROPEP 21 318
CC FT CHAIN 319 427
CC FT DISULFID 325 391
CC FT DISULFID 354 424
CC FT DISULFID 358 426
CC FT DISULFID 390 426
CC FT CARBOHYD 71 71
CC FT CARBOHYD 136 136
CC FT CARBOHYD 265 265
CC FT CARBOHYD 292 292
CC FT CARBOHYD 48626 MW; 23AA42DC0785FABC CRC64;
CC
CC SEQUENCE 427 AA; 48626 MW; 23AA42DC0785FABC CRC64;
CC
CC
CC Query Match 59.1%; Score 808.5; DB 1; Length 427;
CC Best Local Similarity 61.9%; Pred. No. 1.5e-64;
CC Matches 161; Conservative 31; Mismatches 59; Indels 9; Gaps 5;

```

```

QY 178 EYDAEKGCGFFPLADVPTTKAIVQTLVHLKFTKYGKACCVPTLSPLSTIKYDDM 237
DB 348 DYAEKCGGCGFFPLTNVPTTKAIVQTLVHLNDRKSKACCVPTLDAISILYKDDA 407
QY 238 GVPFLTYHYEGSMGSAVEGCCR 257
DB 408 GVPFLTYHYEGSMGSAVEGCCR 427

```

RESULT 4

BM10_HUMAN STANDARD; PRT; 424 AA.

AC 095393;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DE 15-JUN-2002 (Rel. 41, Last annotation update)

DE Bone morphogenetic protein 10 precursor (BMP-10).

GN BMP10.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Celeste A.J.;

RT "Homo sapiens bone morphogenetic protein 10 (BMP-10) mRNA.";

RT Submitted (OCT-1998) to the EMBL/Genbank/DBJ databases.

CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).

CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

CC -----

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CC or send an email to license@isb-sib.ch).

CC

CC EMBL: AF101441; AAC7462.1; -.
CC HSSP: P12643; 3BMP.
CC
CC InterPro: IPR002405; Inhibin_alpha.
CC
CC InterPro: IPR001839; TGFb.
CC
CC InterPro: IPR001111; TGFb_N.
CC
CC Pfam: PF000019; TGF-beta; 1.
CC
CC Pfam: PF00688; TGFb_propeptide; 1.
CC
CC PRINTS: PR00669; INHIBIN.
CC
CC ProDom: PD000357; TGFb; 1.
CC
CC SMART: SM00204; TGFb; 1.
CC
CC PROSITE: PS00250; TGF_BETA_1; 1.
CC
CC Signal: Growth factor; Cytokine; Glycoprotein.
CC
CC FT SIGNAL 1 21
CC FT PROPEP 22 316
CC FT CHAIN 317 424
CC FT DISULFID 323 389
CC FT DISULFID 352 421
CC FT DISULFID 356 423
CC FT DISULFID 388 423
CC FT CARBOHYD 67 67
CC FT CARBOHYD 131 131
CC FT CARBOHYD 48047 MW; 3FDB3B7221BB2254 CRC64;
CC
CC SEQUENCE 424 AA; 48047 MW; 3FDB3B7221BB2254 CRC64;
CC
CC
CC Query Match 37.8%; Score 516.5; DB 1; Length 424;
CC Best Local Similarity 42.8%; Pred. No. 1.5e-38;
CC Matches 119; Conservative 48; Mismatches 68; Indels 43; Gaps 11;

Db 226 SKHDEADASSGRLEIDPTSAQNHNPILLIVFSDQGS--SDKERKEELNEMISHEDLPET- 282
 QY 114 KTKAKNAYGAGESEGEELDOSTYAVGP-----LLARRK-----RSTGSSHCQKTS 159
 Db 283 -----DNIGLSDFSS-GPGEALLOMSNIIYDSTARIRAKNAGNCKTKPT 327
 QY 160 LKVNEDIGWDSWIIAPKREYDAVECKGCFPLADVPTPKHAIYVTLVHLKFPKTVKGA 219
 Db 328 LYIDKEIGWDSWIIAPKREYDAVECKGCFPLADVPTPKHAIYVTLVHLKFNKSKASKA 387
 QY 220 CCVPTKLPISILYKDDMGVPTLKYHEGMSVAECCGR 257
 Db 388 CCVPTKLPISILYKDDMGVPTLKYHEGMSVAECCGR 424

RESULT 5
 BM10_MOUSE STANDARD; PRT; 420 AA.
 AC 09R229; 09218; 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Bone morphogenetic protein 10 precursor (BMP-10).
 GN BMP10.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10990;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NH Swiss;
 RX MEDLINE=99173786; PubMed=10072785;
 RA Neuhaus H., Rosen V., Thies R.S.;
 RT "Heart specific expression of mouse BMP-10 a novel member of the TGF-
 beta superfamily.";
 RL Mech. Dev. 80:181-184(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Celeste A.;
 RT "Mouse bone morphogenetic protein 10 (BMP-10) genomic sequence, full
 coding region of exon 2.";
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 CC -1-SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
 CC -1-SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1-TISSUE SPECIFICITY: HEART-SPECIFIC.
 CC -1-SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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 CC -----
 CC EMBL; AF101033; AAC95357.1; -;
 DR EMBL; AF101440; AAC77461.1; -;
 DR EMBL; AF101439; AAC77461.1; JOINED.
 DR HSSP; P12643; 3BMP.
 DR MGD; MGI:1338820; Bmp10.
 DR InterPro; IPR002405; Tnhb1n.alpha.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb.N.
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR PRINTS; PR00669; INHIBINA.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Signal; Growth factor; Cytokine; Glycoprotein.
 FT SIGNAL 1 21
 FT PROPEP 22 312
 FT CHAIN 313 420 BONE MORPHOGENETIC PROTEIN 10.

FT DISULFID 319 385 BY SIMILARITY.
 FT DISULFID 348 417 BY SIMILARITY.
 FT DISULFID 352 419 BY SIMILARITY.
 FT DISULFID 384 384 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 67 67 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 130 130 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 111 111 E -> ED (IN REF. 2).
 SQ SEQUENCE 420 AA; 47802 MW; 724EC0D4C4CF0B4 CRC64;
 Query Match 37.1%; Score 507; DB 1; Length 420;
 Best Local Similarity 42.5%; Pred. No. 1e-37;
 Matches 116; Conservative 49; Mismatches 72; Indels 36; Gaps 11;
 QY 1 DYLEDSEWMDATGKTFLVSQDI--RDEGWELEYSNAKRVARDSTTKNKKLEYVQ 58
 Db 168 EVLESADGSEER-SMLVSTEIYGTNSSEFEDYDAIRWQKGPST--HGLEIHE 224
 QY 59 SHRESCD-----TLDISVPGSKMLPFVYFSDNSNGYETRLDLKEMIGHDEFTMLV 113
 Db 225 SRQNAEDTGRQLEIDMSAQNHDPILLYVFSDDQS-DKECK-DELNLITHEDDLDD 282
 QY 114 KTKAKNAYGAGESEGEEL-----DGYTAVGPLARRKSTGASSHCQKTSLRNF 164
 Db 283 SDA--FFSG---PDEEALLOMSNMIDDSST-----RIRNAKGYCKKPTLYTDF 328
 QY 165 EDIGWDSWIIAPKREYDAVECKGCFPLADVPTPKHAIYVTLVHLKFPKTVKACVPT 224
 Db 329 KEIGWDSWIIAPKREYDAVECKGCFPLADVPTPKHAIYVTLVHLKFNKSKASKA 387
 QY 225 KLSPTSLYKDDMGVPTLKYHEGMSVAECCGR 257
 Db 389 KLDPSILYL-DKGVVYTKFYKFGMAVSECCGR 420

RESULT 6
 BMP4_HUMAN STANDARD; PRT; 408 AA.
 AC P12644; 09JUN80; 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Bone morphogenetic protein 4 precursor (BMP-4).
 GN BMP4 OR BMP2B OR DVK4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89072730; PubMed=3201241;
 RA Wozney J.M., Rosen V., Celeste A.J., Mitscock L.M., Whitters M.J.,
 RA Kriz R.W., Hewick R.M., Wang E.A.;
 RT "Novel regulators of bone formation: molecular clones and
 activities.";
 RL Science 242:1528-1534(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98368971; PubMed=9701626;
 RA Shore E.M., Xu M., Shah P.B., Janoff H.B., Hahn G.V., Deardorff M.A.,
 RA Sovinsky L., Spliner N.B., Zasloff M.A., Wozney J.M., Kaplan F.S.;
 RT "The human bone morphogenetic protein 4 (BMP-4) gene: molecular
 structure and transcriptional regulation.";
 RL Calcif. Tissue Int. 63:221-229(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Duodenum;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 7-408 FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=96063017; PubMed=7579580;
 RA Oida S., Iimura T., Maruoka Y., Takeda K., Sasaki S.;


```
RT      *Cloning and sequence of bone morphogenetic protein 4 (BMP-4) from a
RL      human placental cDNA library.
CC      DNA Seq. 5:273-275(1995).
CC      -1- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION. ALSO ACT IN
CC      MESODERM INDUCTION, TOOTH DEVELOPMENT, LIMB FORMATION AND FRACTURE
CC      REPAIR.
CC      -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: SECRETED INTO THE EXTRACELLULAR MATRIX.
CC      -1- TISSUE SPECIFICITY: EXPRESSED IN THE LUNGS AND LOWER LEVELS SEEN
CC      IN THE KIDNEY. PRESENT ALSO IN NORMAL AND NEOPLASTIC PROSTATE
CC      TISSUES. AND PROSTATE CANCER CELL LINES.
CC      -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC      -----
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CC      or send an email to license@sib-sib.ch).
CC      -----
DR      EMBL; M22490; AAC51835.1; -
DR      EMBL; U43842; AAC72278.1; -
DR      EMBL; BC020546; AAH20546.1; -
DR      PIR; D30751; BAA06410.1; -
DR      PIR; C37278; C37278.
DR      HSP; P12643; 3BMP.
DR      Genew; HGNC:1071; BMP4.
DR      MIM; 112262; -
DR      InterPro; IPR001839; TGFb.
DR      InterPro; IPR001111; TGFb_N.
DR      Pfam; PF000688; TGFb-propeptide; 1.
DR      ProDom; PD000357; TGFb; 1.
DR      SMART; SM00204; TGFb; 1.
DR      PROSITE; PS00250; TGF-BETA_1; 1.
DR      KMW; Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
FT      SIGNAL 1 19
FT      PROPEP 20 292
FT      CHAIN 293 408
FT      DISULFID 308 373
FT      DISULFID 337 405
FT      DISULFID 341 407
FT      DISULFID 372 372
FT      CARBOHYD 143 143
FT      CARBOHYD 208 208
FT      CARBOHYD 350 350
FT      CARBOHYD 365 365
FT      CONFLICT 152 152
SQ      SEQUENCE 408 AA; 46555 MW; 79B01179DBB98204 CRC64;
Query Match 25.2%; Score 345; DB 1; Length 408;
Best Local Similarity 33.9%; Pred. No. 2,7e-23;
Matches 83; Conservative 28; Mismatches 76; Indels 48; Gaps 7;
QY 29 WETLEVSAAVKRWRAVDSTNNKMLEVT-----VQSHRSCDTLDISVPGSKN---LPF 80
DB 212 WETFDVSPAVLRMTREKQRYGLAIVETHLHOTRTNHCQHVRISSLPQSGGNAQRLP 271
QY 81 FVFSNSNRSGTETRLDLKEMIGHQETMLVYTKAKNAYOGAGSGQSEBGLDGYTAGVP 140
DB 272 LVTFGHQ-GRGHALTRRRRRKRSRPHNSQR----- 300
QY 141 LLARRKSTGASHCOKTSLRVNFEDIGDMSWLIAPKEVDAYECKGCGFPPLADVPTK 200
DB 301 --ARRK-----NKNCRHSLYVDFSDVGWMDVIAPRGVQAYCHGDCRPFPLADHLNSTN 353
QY 201 HAIYOTLVHLKFTPKYKACGCVPTKSPISILYKDDMGVPTLKITYEEMASVABEGCR 257
DB 354 HAIYOTLVN-SVNSSIPKACCVPTELSTALSMLEYLDYDKVLK-NYQEMVVEGGCR 408
RESULT 7
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```
BMP4_RAT
ID      BMP4_RAT          STANDARD:      PRT:      408 AA.
AC      006826;
DT      01-JUN-1994 (Rel. 29, Created)
DT      01-JUN-1994 (Rel. 29, last sequence update)
DT      16-OCT-2001 (Rel. 40, last annotation update)
DE      Bone morphogenetic protein 4 precursor (BMP-4) (BMP-2B).
CN      BMP4 OR BMP-4 OR DVR-4.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=93385158; PubMed=8373807;
RA      Chen D., Feng J.O., Peng M., Harris M.A., Mundy G.R., Harris S.F.;
RT      "Cloning and sequence of bone morphogenetic protein 4 cDNA from fetal
RT      rat calvarial cell.";
RL      Biochim. Biophys. Acta 1174:289-292(1993).
CC      -1- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
CC      -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: SECRETED INTO THE EXTRACELLULAR MATRIX.
CC      -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC      -----
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CC      or send an email to license@sib-sib.ch).
CC      -----
DR      EMBL; Z23607; CAAB8329.1; -
DR      PIR; S33173; S33173.
DR      PIR; S38343; S38343.
DR      HSP; P12643; 3BMP.
DR      InterPro; IPR001839; TGFb.
DR      InterPro; IPR001111; TGFb_N.
DR      Pfam; PF000688; TGFb-propeptide; 1.
DR      ProDom; PD000357; TGFb; 1.
DR      SMART; SM00204; TGFb; 1.
DR      PROSITE; PS00250; TGF-BETA_1; 1.
DR      KMW; Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
FT      SIGNAL 1 19
FT      PROPEP 20 292
FT      CHAIN 293 408
FT      DISULFID 308 373
FT      DISULFID 337 405
FT      DISULFID 341 407
FT      DISULFID 372 372
FT      CARBOHYD 144 144
FT      CARBOHYD 209 209
FT      CARBOHYD 350 350
FT      CARBOHYD 365 365
SQ      SEQUENCE 408 AA; 46540 MW; 61E924B8BD5624F3 CRC64;
Query Match 25.0%; Score 342.5; DB 1; Length 408;
Best Local Similarity 35.4%; Pred. No. 4,5e-23;
Matches 84; Conservative 31; Mismatches 73; Indels 49; Gaps 7;
QY 29 WETLEVSAAVKRWRAVDSTNNKMLEVT-----VQSHRSCDTLDISVPGSKN---LPF 80
DB 213 WETFDVSPAVLRMTREKQRYGLAIVETHLHOTRTNHCQHVRISSLPQSGGNAQRLP 272
QY 81 FVFSNSNRSGTETRLDLKEMIGHQETMLVYTKAKNAYOGAGSGQSEBGLDGYTAGVP 140
DB 273 LVTFGHQGR-----GH---TLTRRRKRSRPHNSQR----- 295
QY 141 LLARRKSTGASHCOKTSLRVNFEDIGDMSWLIAPKEVDAYECKGCGFPPLADVPTK 200
DB 296 --HHQSRKRNKNCRRHSLYVDFSDVGWMDVIAPRGVQAYCHGDCRPFPLADHLNSTN 353
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OY 201 HAIVOTLVHLKFPYKVGACVPTKLSPIISILYKDDMGVPTLKYHSGSVAECCGR 257
DB 354 HAIVOTLVN-SVNSSIPKACCVPTLSAISMLYIDEYDKVYLK-NYQENYVEGCCCR 408

RESULT 8
BMP4_DAMDA STANDARD; PRT; 408 AA.
ID BMP4_DAMDA Q29607;
AC 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
GN Bone morphogenetic protein 4 precursor (BMP-4).
OS Dama dama (Fallow deer) (Cervus dama).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=30532;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Antler;
RX MEDLINE=95367593; PubMed=7640308;
RA Feng J.O., Chen D., Esparea J., Harris M.A., Mundy G.R.,
RA Harris S.E.;
RT "Deer antler tissue contains two types of bone morphogenetic protein
RT 4 mRNA transcripts."
RL Biochim. Biophys. Acta 1263:163-168(1995).
CC -1- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL: S79174; AAA80514.1; -.
DR HSSP: P12643; 3BMP.
DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001111; TGFb.N.
DR Pfam: PF00019; TGF-beta: 1.
DR Pfam: PF00688; TGFb.propeptide; 1.
DR ProDom: PD000357; TGFb; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF_BETA_1; 1.
KW Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
FT SIGNAL 1 19
FT PROPEP 20 292
FT CHAIN 293 408
FT DISULFD 308 373
FT DISULFD 337 403
FT DISULFD 341 407
FT DISULFD 372 372
FT CAROHRD 144 144
FT CAROHRD 208 208
FT CAROHRD 350 350
FT CAROHRD 365 365
SQ SEQUENCE 408 AA; 46563 MW; 17BA333BB11226FA CRC64;

Query Match 24.98; Score 341; DB 1; Length 408;
Best Local Similarity 35.98; Pred. No. 6.1e-23;
Matches 85; Conservative 31; Mismatches 73; Indels 48; Gaps 8;
OY 29 WETLVSASVAVRWADSTNKNKLEVT-----VQSHRESODTLDISVPGSKN-----LPF 80
DB 212 WETPVSAYLVKRWREKOPNGLAIEVTHLHQRTHOGQHVRIKSLPQSGSDMAQLRPL 271
OY 81 FVVSFNSDNGSTKTRDLKLEMGIEQETMLVKTAKMAYOGAGSQESEGIDGTVAVP 140

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DB 272 LVTFGHDR-----GH-----ALTRHRAKRSKHH-----P 298
OY 141 LIAARRKSTGASSHCOKTSILRVNFDIGDMSWIIAPKEVDAYACKGCFFPLADDVTPK 200
DB 299 QRAKKR-----KNCRNRISLVYDSDVGNMWIYAPGYOAFYCHDCDFPLADHINSTN 353
OY 201 HAIVOTLVHLKFPYKVGACVPTKLSPIISILYKDDMGVPTLKYHSGSVAECCGR 257
DB 354 HAIVOTLVN-SVNSSIPKACCVPTLSAISMLYIDEYDKVYLK-NYQENYVEGCCCR 408

RESULT 9
BMP4_MOUSE STANDARD; PRT; 408 AA.
ID BMP4_MOUSE P21275;
AC 01-MAY-1991 (Rel. 18, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
GN Bone morphogenetic protein 4 precursor (BMP-4) (BMP-2b).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Dickinson M.E., van der Meer-De Jong R., Hogan B.L.M.;
RL Submitted (xxx-1992) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93282803; PubMed=8507180;
RA Kurihara T., Kitamura K., Takaoka K., Nakazato H.;
RT "Murine bone morphogenetic protein-4 gene: existence of multiple
RT promoters and exons for the 5'-untranslated region."
RL Biochem. Biophys. Res. Commun. 192:1049-1056(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93365172; PubMed=8358941;
RA Takaoka K., Yoshikawa H., Hasimoto J., Masuhara K., Miyamoto S.,
RA Suzuki S., Ono K., Matsui M., Oikawa S., Tsuruoka N.;
RT "Gene cloning and expression of a bone morphogenetic protein derived
RT from a murine osteosarcoma."
RL Clin. Orthop. Relat. Res. 294:344-352(1993).
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=129/Sv; TISSUE=Liver;
RX MEDLINE=96081880; PubMed=7499338;
RA Feng J.O., Chen D., Cooney A.J., Tsai M., Harris M.A., Tsai S.Y.,
RA Feng M., Mundy G.R., Harris S.E.;
RT "The mouse bone morphogenetic protein-4 gene: Analysis of promoter
RT utilization in fetal rat calvarial osteoblasts and regulation by
RT Coup-TF1 orphan receptor."
RL J. Biol. Chem. 270:28364-28373(1995).
RN [5]
RP SEQUENCE OF 241-408 FROM N.A.
RX MEDLINE=90228966; PubMed=1970330;
RA Dickinson M.E., Kobrin M.S., Silan C.M., Kingsley D.M., Justice M.J.,
RA Miller D.A., Cegi J.D., Lock L.F., Lee A., Buchberg A.M.,
RA Siracusa L.D., Lyons K.M., Derynck R., Hogan B.L.M., Copeland N.G.,
RA Jenkins N.A.;
RT "Chromosomal localization of seven members of the murine TGF-beta
RT superfamily suggests close linkage to several morphogenetic mutant
RT loci."
RL Genomics 6:505-520(1990).
CC -1- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: SECRETED INTO THE EXTRACELLULAR MATRIX.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X56848; CAA40179.1; -
 DR EMBL: S65032; AAB28021.1; -
 DR EMBL: L47480; AAC37698.1; ALT_INIT.
 DR EMBL: D14814; BAA03555.1; -
 DR PIR: B34201; B34201.
 DR PIR: S29523; S29523.
 DR HSP: P12643; 3BMP.
 DR MGD: MGI:88180; Bmp4.
 DR InterPro: IPR001839; TGFb.
 DR InterPro: IPR001111; TGFb_N.
 DR Pfam: PF00019; TGF-beta; 1.
 DR Pfam: PF00688; TGFb.propeptide; 1.
 DR ProDom: PD000357; TGFb; 1.
 DR SMART: SM00204; TGFb; 1.
 DR PROSITE: PS00250; TGF-BETA.1; 1.
 DR Signal: Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
 KW SIGNAL 1 19
 FT PROPEP 20 292
 FT CHAIN 293 408 BONE MORPHOGENETIC PROTEIN 4.
 FT DISULFID 308 373 BY SIMILARITY.
 FT DISULFID 337 405 BY SIMILARITY.
 FT DISULFID 341 407 BY SIMILARITY.
 FT DISULFID 372 372 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 209 209 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 365 365 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 407 407 C -> S (IN REF. 2).
 SO SEQUENCE 408 AA; 46496 MW; 35053D844624EFD0 CRC64;
 Query Match 24.7%; Score 337.5; DB 1; Length 408;
 Best Local Similarity 35.0%; Pred. No. 1.2e-22;
 Matches 83; Conservative 32; Mismatches 73; Indels 49; Gaps 7;
 QY 29 WETLEVSAAKRVNADSTNNKLEVT---VQSHRESCTLDISVPPGSKN---LPF 80
 Db 213 WETFDVSPAVLWRTREKOPNYGLAIEVTHLQTRHOGVHRISLSLQSGDMAOQLRPL 272
 QY 81 FVFSNDRSGTKETRLDLKEMIGHEDETMVYKTAKNAYOGAGSEQDEESLDGYTAVGP 140
 Db 273 LVTFGHGCR-----GH---TLTRRAKRSKPK----- 295
 QY 141 LLARKRSTGASHCOCTSLRVNFEEDIGDMSWIIAPKEYDAYECKGCGFFPLADVPTK 200
 Db 296 --HHQGRSKKNNKCRHSLYDFSDVGNDMTIVAPGVQAFYCHGDCRPFPLADHLNSTN 353
 QY 201 HAIYQTLVHLKFTPKYKACVPTKLSPISTILYKDDMGVPLTKYHEGMSVAEGCGR 257
 Db 354 HAIYQTLVN--SVNSSIPKACVPTLSALSMYLDEYKVYK--NYQENVEEGCGCR 408
 RESULT 10
 BMP4_RABIT
 ID BMP4_RABIT STANDARD; PRT; 409 AA.
 AC 046576;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Bone morphogenetic protein 4 precursor (BMP-4).
 GN BMP4 OR BMP-4.
 OS Oryctolagus cuniculus (Rabbit).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 CX NCBI_TaxID:9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-New Zealand white; TISSUE-Ocular ciliary epithelium;
 RA Wan X.L., Sears J., Chen S., Sears M.;
 RT "Cloning and expression of BMP-2/-4 from rabbit ocular ciliary

RT epithelium.";
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION (BY SIMILARITY).
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: SECRETED INTO THE EXTRACELLULAR MATRIX.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AF042497; AAB97467.1; -
 DR HSP: P12643; 3BMP.
 DR InterPro: IPR001839; TGFb.
 DR InterPro: IPR001111; TGFb_N.
 DR Pfam: PF00019; TGF-beta; 1.
 DR Pfam: PF00688; TGFb.propeptide; 1.
 DR ProDom: PD000357; TGFb; 1.
 DR SMART: SM00204; TGFb; 1.
 DR PROSITE: PS00250; TGF-BETA.1; 1.
 DR Signal: Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
 KW SIGNAL 1 19
 FT PROPEP 20 293
 FT CHAIN 294 409 BONE MORPHOGENETIC PROTEIN 4.
 FT DISULFID 309 374 BY SIMILARITY.
 FT DISULFID 338 406 BY SIMILARITY.
 FT DISULFID 342 408 BY SIMILARITY.
 FT DISULFID 373 373 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 209 209 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 351 351 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SO SEQUENCE 409 AA; 46641 MW; 35557561447AD635 CRC64;
 Query Match 24.6%; Score 336; DB 1; Length 409;
 Best Local Similarity 35.4%; Pred. No. 1.7e-22;
 Matches 84; Conservative 29; Mismatches 76; Indels 48; Gaps 7;
 QY 29 WETLEVSAAKRVNADSTNNKLEVT---VQSHRESCTLDISVPPGSKN---LPF 80
 Db 213 WETFDVSPAVLWRTREKOPNYGLAIEVTHLQTRHOGVHRISLSLQSGDMAOQLRPL 272
 QY 81 FVFSNDRSGTKETRLDLKEMIGHEDETMVYKTAKNAYOGAGSEQDEESLDGYTAVGP 140
 Db 273 LVTFGHGCR-----GH---TLTRRAKRSKPK-----P 299
 QY 141 LLARKRSTGASHCOCTSLRVNFEEDIGDMSWIIAPKEYDAYECKGCGFFPLADVPTK 200
 Db 300 QRAKK-----NKKCRHSLYDFSDVGNDMTIVAPGVQAFYCHGDCRPFPLADHLNSTN 354
 QY 201 HAIYQTLVHLKFTPKYKACVPTKLSPISTILYKDDMGVPLTKYHEGMSVAEGCGR 257
 Db 355 HAIYQTLVN--SVNSSIPKACVPTLSALSMYLDEYKVYK--NYQENVEEGCGCR 409
 RESULT 11
 GDF6_BOVIN
 ID GDF6_BOVIN STANDARD; PRT; 436 AA.
 AC P55106;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Growth/differentiation factor 6 precursor (GDF-6) (cartilage-derived
 DE morphogenetic protein 2) (CDMP-2) (Fragment).
 GN GDF6 OR CDMP2.
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Bovinae; Bos.

```

OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Articular cartilage;
RX MEDLINE=95050604; PubMed=7961761;
RA Chang S., Hoang B., Thomas J.T., Vukicevic S., Luyten F.P.,
RA Ryba N.J.P., Kozak C.A., Reddi A.H., Moos M.;
RT Cartilage-derived morphogenetic proteins. New members of the
RT transforming growth factor-beta superfamily predominantly expressed
RT in long bones during human embryonic development.;
RL J. Biol. Chem. 269:28227-28234(1994).
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U13661; AAA61416.1; -.
DR HSSP: P18075; 1BMP.
DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001111; TGFb.N.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGFb.propeptide; 1.
DR ProDom: PD000357; TGFb; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF_BETA_1; 1.
DR Growth factor; Cytokine; Glycoprotein.
KW NON_TER
FT PROPEP 1 316 POTENTIAL.
FT CHAIN 317 436 GROWTH/DIFFERENTIATION FACTOR 6.
FT DISULFD 335 401 BY SIMILARITY.
FT DISULFD 364 433 BY SIMILARITY.
FT DISULFD 368 435 BY SIMILARITY.
FT DISULFD 400 400 INTERCHAIN (BY SIMILARITY).
FT CAROHYD 27 27 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 436 AA; 47873 MW; B0688E12EF8AE91D CRC64;

Query Match 24.1%; Score 330; DB 1; Length 436;
Best Local Similarity 36.7%; Pred. No. 6.3e-22;
Matches 81; Conservative 23; Mismatches 67; Indels 50; Gaps 7;

QY 72 PGSKNLP-----FVFSNDRSNGTKETRLDLKEMIGHQETMLVYTKANA 119
DB 231 PDLRSLGGRKVRTPQERALLVFSRSQ-----RKTFLAEMREOLGSALEYV----- 278
QY 120 YGAGESEEE-----LDGYTAG-----PLARRKSTGASSH-----CQ 156
DB 279 --GPGGAGSGSPPPPPPPPPSTPDAGLMSFSPGRKRRRTAASHGRHKKRKLK 336
QY 157 KTSLVNFEIDGWSMIAPREYDAECKGCEFPPLADDTPTKNAIVQTLVHLKPTKV 216
DB 337 KRPPLVNFELGMDMIAPLEAYHCEGVCDFPLRSHLEPTNHAIIOTLMSMDPGST 396
QY 217 GKACCVPTKLPISILYKDMGVPTLKYHKGMSVAECGR 257
DB 397 PSCCVPTKLPISILY-IDAGNNVNYNEIEYVESCGR 436

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OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White leghorn;
RX MEDLINE=94163974; PubMed=8119128;
RA Francis P.H., Richardson M.K., Brickle P.M., Tickle C.;
RT Bone morphogenetic proteins and a signalling pathway that controls
RT patterning in the developing chick limb.;
RL Development 120:209-218(1994).
RN [2]
RP FUNCTION.
RX MEDLINE=99128179; PubMed=9927590;
RA Pizette S., Misanader L.;
RT BMs negatively regulate structure and function of the limb apical
RT ectodermal ridge.;
RL Development 126:883-894(1999).
CC -1- FUNCTION: NEGATIVELY REGULATES THE STRUCTURE AND FUNCTION OF THE
CC LIMB APICAL ECTODERMAL RIDGE.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL: X75915; CA53514.1; -.
DR HSSP: P12643; 3BMP.
DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001111; TGFb.N.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGFb.propeptide; 1.
DR ProDom: PD000357; TGFb; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF_BETA_1; 1.
DR Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
KW SIGNAL
FT PROPEP 1 291 POTENTIAL.
FT CHAIN 292 405 BONE MORPHOGENETIC PROTEIN 4.
FT DISULFD 305 370 BY SIMILARITY.
FT DISULFD 334 402 BY SIMILARITY.
FT DISULFD 338 404 BY SIMILARITY.
FT DISULFD 369 369 INTERCHAIN (BY SIMILARITY).
FT CAROHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 208 208 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 347 347 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 362 362 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 405 AA; 46057 MW; 54302BDA04081 CRC64;

Query Match 23.9%; Score 327.5; DB 1; Length 405;
Best Local Similarity 33.2%; Pred. No. 9.6e-22;
Matches 79; Conservative 36; Mismatches 70; Indels 53; Gaps 7;

QY 29 WETLEVSAYKRWYAADSTKNKLEYT-----VQSRRESODTLDISVPG-----SKNLP 79
DB 212 WETFDVSPAVIRWTKDKOPNGLVETHLHQQTGQKRVRSNLSFGHGGDMAQLRP 271
QY 80 FVFSNDRSNGTKETRLDLKEMIGHQETMLVTKANA YGAGESEEEGLDGYTAG 139
DB 272 LVYTFGHDR-----GH-----ALTRRRARSPKHGGRKKK----- 303
QY 140 PLLARRKSTGASSHCKTSLRVNFEIDGWSMIAPREYDAECKGCEFPPLADDTPT 199
DB 304 -----NCRNHAIYDFSDVGNMDIVAPPGTQATYCGDCFPPLADHLNST 349
QY 200 KNAIVQTLVHLKFPYKVGACVPTKLPISILYKDMGVPTLKYHKGMSVAECGR 257

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Db          350 NHAIVOTLVN-SVNSIPKACCVPELTAISIMLYDEDKYVLK-NYEEMVVEGCCR      405
||||| : : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
||||| : : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :

RESULT 13
-----
ID DECA_DROME STANDARD: PRT; 568 AA.
AC P07713; P91651.
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Dccpentaplegic protein precursor (DPP-C protein).
GN DPP.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachyera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87090408; PubMed=3467201.
RA Padgett R.W., St Johnston R.D., Gelbart W.M.;
RT "A transcript from a drosophila pattern gene predicts a protein homologous to the transforming growth factor-beta family." ; Nature 325:81-84(1987).
RL [2]
RN RP SEQUENCE FROM N.A.
RX STRAIN-DP CN BW;
RC MEDLINE=97225213; PubMed=9071586;
RA Richter B., Long M., Lewontin R.C., Nilasaka E.;
RT "Nucleotide variation and conservation at the dpp locus, a gene controlling early development in Drosophila." ; Genetics 145:311-323(1997).
RL [3]
CN CHARACTERIZATION, AND SEQUENCE OF 457-476.
RX MEDLINE=90258653; PubMed=1692958;
RA Pangonibn G.E.F., Rashtka K.E., Neitzel M.D., Hoffmann F.M.;
RT "Biochemical characterization of the Drosophila dpp protein, a member of the transforming growth factor beta family of growth factors." ; Mol. Cell. Biol. 10:2669-2677(1990).
CL -1- FUNCTION: ACTS AS AN EXTRACELLULAR MORPHOGEN TO ESTABLISH AT LEAST TWO CELLULAR RESPONSE THRESHOLDS WITHIN THE DORSAL HALF OF THE DROSOPHILA EMBRYO. REQUIRED FOR THE PROPER DEVELOPMENT OF THE EMBRYONIC DORSAL HYPODERM. FOR VIABILITY OF LARVAE AND FOR CELL VIABILITY OF THE EPITHELIAL CELLS IN THE IMAGINAL DISKS. ACTS TOGETHER WITH SCW.
CC -1- SUBUNIT: HETERODIMERS OF SCW/DPP ARE THE ACTIVE SUBUNIT, DPP/DPP HOMODIMERS ELICIT A BASAL RESPONSE AND SCW/SCW HOMODIMERS ALONE ARE INTERACTIVE IN EXPRESSING A DORSAL PATTERN.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE IMAGINAL DISCS ASSOCIATED WITH ESTABLISHMENT OF THE PROXIMAL-DISTAL AXIS OF THE APPENDAGES, AND MIDCUT MESODERM.
CC CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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EMBL, M30115; AAA28482.1; -.
DR EMBL, U63857; AAC47552.1; -.
DR PIR, A26158; A26158.
DR HSSP, P12643; 3BMP.
DR FlyBase; FBgn0000490; dpp.
DR InterPro; IPR001839; TGFB.
DR InterPro; IPR001111; TGFB_N.
DR Pfam; PF000019; TGF-beta_1.
DR pfam; PF000686; TGfb-Propeptide; 1.
DR ProDom; PD000357; TGFB; 1.
DR SMART; SM00204; TGFb; 1.

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DR	PROSITE:PS00250; TGF_BETA.1; 1.	KW	Growth factor; Developmental protein; Differentiation; Glycoprotein;
FT	SIGNAL.	1	POTENTIAL.
FT	PROPEP	16	456
FT	CHAIN	457	588
FT	DISULFID	487	553
FT	DISULFID	516	585
FT	DISULFID	520	587
FT	CARBOHYD	552	552
FT	CARBOHYD	120	120
FT	CARBOHYD	342	342
FT	CARBOHYD	377	377
FT	CARBOHYD	529	529
FT	VARIANT	59	59
FT	VARIANT	121	121
FT	VARIANT	473	474
SO	SEQUENCE	588 AA;	65850 MW; 3D986A7DE5DE666B CRC64;
Query Match		23.8%;	Score 325; DB 1; Length 588;
Best Local Similarity		30.5%;	Pred. No. 2.6e-21;
Matches	92;	Conservative	45; Mismatches 115; Indels 50; Gaps
QY	4	EDEETDQATGTKTFPLVSODIR---	DEGWETLEY---SSAVKRWYRADSTGNKKLEY 55
Db	289	KDSKIDRFPHNHRRFLHDYKSIPIADEKILAAEQLTIRDLASQVAVSSSSANRRYQV 348	
QY	56	T-----VQSRE-----	SCDTDISVPSG-----SKNLPFFVYS 85
Db	349	LYVDITRVGKRGKRGREPSYLLDPTKTVRLNSTDTVSLVDYQAVDWKLASPRQNTGLVEYR 408	
QY	86	NDRS-----	NGTKETRLDLLEKEMIGHEOETMLVTKAKNAVQAGAGEQEEGLDGYTAV 138
Db	409	TVNSLKFAPHHNRHLRRSADENHMOHQRDLTFYTTDGRHK--ARSIRVSGEGGKG 467	
QY	139	GPLLRKRSSTGASNH---COKTSLRVNPEEDIGMWSYLIARKEVDAYEGKGGCFPLAD 195	
Db	468	GRKNRKNRRPTRRKKNNDYDKRHSLLVDFSDGMDWLVVAFLGTDATYCGKCPFLADH 527	
QY	196	VTPKHAIVOTLVHLKFTPKVGKACCPVTKSPISILIKDDMGVPLTKHYHGNVAEG 255	
Db	528	FNSTNHAVVOTLVNMMNPGKVPKACCVPTOLDVSAMLELNDOSTYVVLK-NYQEMTVVGG 586	
QY	256	CR 257	
Db	587	CR 588	
RESULT 14			
DECA-DROPS			
ID	DECA-DROPS	STANDARD:	PRT: 621 AA.
AC	P91699;		
DT	15-DEC-1998 (Rel. 37, Created)		
DT	15-DEC-1998 (Rel. 37, Last sequence update)		
DT	15-DEC-1998 (Rel. 37, Last annotation update)		
DE	Decapentaplegic protein precursor (DPP-C protein).		
GN	DPP.		
OS	Drosophila pseudobscura (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;		
OC	Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;		
OC	Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.		
OX	NCBI_TaxID=7237;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE-97225212; PubMed-9071585;		
RA	Newfield S.J., Padgett R.W., Flindley S.D., Richter B.G., Sanicola M.,		
RA	de Cuevas M., Gelbart W.M.;		
RT	"Molecular evolution at the decapentaplegic locus in Drosophila.";		
RL	Genetics 145:287-309(1997).		
CC	-1- FUNCTION: ACTS AS AN EXTRACELLULAR MORPHOGEN TO ESTABLISH AT LEAST		
CC	TWO CELLULAR RESPONSE THRESHOLDS WITHIN THE DORSAL HALF OF THE		
CC	DROSOPHILA EMBRYO. REQUIRED FOR THE PROPER DEVELOPMENT OF THE		
CC	EMBRYONIC DORSAL HYPODERM, FOR VIABILITY OF LARVAE AND FOR CELL		

ID	DECA_PROSI	STANDARD:	PRT:	593 AA.
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	15-DEC-1998 (Rel. 37, Last annotation update)			
DE	Decapentaplegic protein precursor (DPP-C protein).			
GN	DPP.			
OS	Eukaryota; Simulans (Fruit fly).			
CC	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;			
CC	Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;			
CC	Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.			
CC	NCBI_taxid=7240;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=NET DPL;			
RX	MEDLINE=97225212; PubMed=9071585;			
RA	Newfield S.J., Padgett R.W., Findley S.D., Richter B.G., Sanicola M.,			
RA	de Cuevas M., Gelbart M.M.;			
RT	*Molecular evolution at the decapentaplegic locus in Drosophila.*;			
RL	Genetics 145:297-309(1997).			
CC	-1- FUNCTION: ACTS AS AN EXTRACELLULAR MORPHOGEN TO ESTABLISH AT LEAST			
CC	TWO CELLULAR RESPONSE THRESHOLDS WITHIN THE DORSAL HALF OF THE			
CC	DROSOPHILA EMBRYO. REQUIRED FOR THE PROPER DEVELOPMENT OF THE			
CC	EMBRYONIC DORSAL HYPODERM, FOR VIABILITY OF LARVAE AND FOR CELL			
CC	VIABILITY OF THE EPITHELIAL CELLS IN THE IMAGINAL DISKS. ACTS			
CC	TOGETHER WITH SCW (BY SIMILARITY).			
CC	-1- SUBUNIT: HETERODIMERS OF SCW/DPP ARE THE ACTIVE SUBUNIT. DPP/DPP			
CC	HOMODIMERS ELICIT A BASAL RESPONSE AND SCW/SCW HOMODIMERS ALONE			
CC	ARE INEFFECTIVE IN SPECIFYING A DORSAL PATTERN (BY SIMILARITY).			
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN THE IMAGINAL DISCS ASSOCIATED			
CC	WITH ESTABLISHMENT OF THE PROXIMAL-DISTAL AXIS OF THE APPENDAGES,			
CC	AND MIDGUT MESODERM (BY SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.			
CC	-----			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL: U63854; AAC47554.1; -			
DR	HSSP: P12643; 3BMP.			
DR	FLYbase: Fbgm0015673; Dslm\dpp.			
DR	InterPro: IPR001839; TGFb.			
DR	InterPro: IPR001111; TGFb_N.			
DR	Pfam: PFO00019; TGF-beta; 1.			
DR	Pfam: PF00688; TGFb.propeptide; 1.			
DR	ProDom: PD000357; TGFb; 1.			
DR	SMART: SM00204; TGFb; 1.			
DR	PROSITE, PS00250; TGF-BETA_1; 1.			
KW	Growth factor; Developmental protein; Differentiation; Glycoprotein;			
KW	Signal.			
FT	SIGNAL	1	15	POTENTIAL.
FT	PROPEP	16	461	BY SIMILARITY.
FT	CHAIN	462	593	DECAPENTAPLEGIC PROTEIN.
FT	DISULFID	492	558	BY SIMILARITY.
FT	DISULFID	521	580	BY SIMILARITY.
FT	DISULFID	525	592	BY SIMILARITY.
FT	DISULFID	557	557	INTERCHAIN (BY SIMILARITY).
FT	CARBOHYD	122	122	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	347	347	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	382	382	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	534	534	N-LINKED (GLCNAC. . .) (POTENTIAL).
EQ	SEQUENCE	593 AA;	66248 MW;	POBDB21209F44380 CRC4;
Query Match		23.6%;	Score 323; DB 1;	Length 593;
Best Local Similarity		30.5%;	Pred. No. 3.9e-21;	

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Science 242, 1528-1534, 1988
 A:Title: Novel regulators of bone formation: molecular clones and activities.
 A:Reference number: A37278; MUID:89072730; PMID:3201241

A:Accession: C37278
 A:Molecule type: mRNA
 A:Residues: 1-408 <WC3>
 A:Cross-references: GB:M22490; NID:g179503; PIDN:AAA51835.1; PID:g179504
 C:Gene: GDB:BMP4; BMP2B
 A:Cross-references: GDB:125205; OMIM:112262
 A:Map position: 14q22-14q23
 C:Superfamily: Inhibin

C:Keywords: bone; glycoprotein
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-292/Domain: propeptide #status predicted <PRO>
 F:293-408/Product: bone morphogenetic protein 4 #status predicted <MTP>
 F:143,208,350,365/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 25.28; Score 345; DB 2; Length 408;
 Best Local Similarity 35.98; Pred. No. 4.5e-22;
 Matches 85; Conservative 28; Mismatches 76; Indels 48; Gaps 7;

QY 29 WETLEVSAAVKRWVRAADSTTNKKNLEVT---VQSHRESCDTLDISVPPGSKN---LPF 80
 DB 212 WETLEVSAAVKRWVRAADSTTNKKNLEVT---VQSHRESCDTLDISVPPGSKN---LPF 80
 QY 81 FVVFNSDSSNGTKETRLDLKEMIGHEQETMLVKTAKNAVQAGSEGEEDGDTTAVGP 140
 DB 272 LVTFEHD-GRGHALTRRRRAKRSKHSOR----- 300
 QY 141 LLARRKSTGASSHCQKTSLVNFEIDIGDMSWIAPEKDAYECKGCGFFPLADDVPTK 200
 DB 301 --ARRK-----NKNCRRHSILVDFSDVGMNDWIVAPPGQAFCHDCDFPLADILNSTN 353
 QY 201 HAIYOTLVHLKFPKRVKACCVPTKLSPIILYKDDMGVPTLKYNHGEKSAVEGCCR 257
 DB 354 HAIYOTLVN-SVNSSIRKACCVPTKLSPIILYKDDMGVPTLKYNHGEKSAVEGCCR 408

RESULT 3

S38343
 bone morphogenetic protein 4 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
 C:Accession: S38343; S33173
 R:Chen, D.; Feng, J.Q.; Feng, M.; Harris, M.A.; Mundy, G.R.; Harris, S.E.
 Blochim. Biophys. Acta 1174, 289-292, 1993
 A:Title: Cloning and sequence of bone morphogenetic protein 4 cDNA from fetal rat calvaria
 A:Reference number: S38343; MUID:93385158; PMID:8373807
 A:Accession: S38343
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-408 <CHD>
 A:Cross-references: EMBL:Z22607; NID:g296856; PIDN:CAA80329.1; PID:g296857
 C:Superfamily: Inhibin

Query Match 25.08; Score 342.5; DB 2; Length 408;
 Best Local Similarity 35.44; Pred. No. 7.5e-22;
 Matches 84; Conservative 31; Mismatches 73; Indels 49; Gaps 7;

QY 29 WETLEVSAAVKRWVRAADSTTNKKNLEVT---VQSHRESCDTLDISVPPGSKN---LPF 80
 DB 213 WETLEVSAAVKRWVRAADSTTNKKNLEVT---VQSHRESCDTLDISVPPGSKN---LPF 80
 QY 81 FVVFNSDSSNGTKETRLDLKEMIGHEQETMLVKTAKNAVQAGSEGEEDGDTTAVGP 140
 DB 273 LVTFEHD-GRGHALTRRRRAKRSKHSOR----- 300
 QY 141 LLARRKSTGASSHCQKTSLVNFEIDIGDMSWIAPEKDAYECKGCGFFPLADDVPTK 200
 DB 296 --HHQSRKRNKNCRRHSILVDFSDVGMNDWIVAPPGQAFCHDCDFPLADILNSTN 353
 QY 201 HAIYOTLVHLKFPKRVKACCVPTKLSPIILYKDDMGVPTLKYNHGEKSAVEGCCR 257

DB 354 HAIYOTLVN-SVNSSIRKACCVPTKLSPIILYKDDMGVPTLKYNHGEKSAVEGCCR 408

RESULT 4

S58791
 bone morphogenetic protein 4 - fallow deer
 C:Species: Dama dama (fallow deer)
 C:Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 16-Feb-1997
 C:Accession: S58791
 R:Feng, J.Q.; Chen, D.; Esparza, J.; Harris, M.A.; Mundy, G.R.; Harris, S.E.
 Blochim. Biophys. Acta 1263, 163-168, 1995
 A:Title: Deer antler tissue contains two types of bone morphogenetic protein 4 mRNA
 A:Reference number: S58791; MUID:95367593; PMID:7640308
 A:Accession: S58791
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-408 <FEN>
 C:Superfamily: Inhibin

Query Match 24.98; Score 341; DB 2; Length 408;
 Best Local Similarity 35.98; Pred. No. 1e-21; 73; Indels 48; Gaps 8;

QY 29 WETLEVSAAVKRWVRAADSTTNKKNLEVT---VQSHRESCDTLDISVPPGSKN---LPF 80
 DB 212 WETLEVSAAVKRWVRAADSTTNKKNLEVT---VQSHRESCDTLDISVPPGSKN---LPF 80
 QY 81 FVVFNSDSSNGTKETRLDLKEMIGHEQETMLVKTAKNAVQAGSEGEEDGDTTAVGP 140
 DB 272 LVTFEHD-GRGHALTRRRRAKRSKHSOR----- 300
 QY 141 LLARRKSTGASSHCQKTSLVNFEIDIGDMSWIAPEKDAYECKGCGFFPLADDVPTK 200
 DB 299 QARRK-----NKNCRRHSILVDFSDVGMNDWIVAPPGQAFCHDCDFPLADILNSTN 353
 QY 201 HAIYOTLVHLKFPKRVKACCVPTKLSPIILYKDDMGVPTLKYNHGEKSAVEGCCR 257
 DB 354 HAIYOTLVN-SVNSSIRKACCVPTKLSPIILYKDDMGVPTLKYNHGEKSAVEGCCR 408

RESULT 5

I49541
 bone morphogenetic protein 4 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
 C:Accession: I49541; S29523; B34201
 R:Feng, J.Q.; Chen, D.; Cooney, A.J.; Tsai, M.; Harris, M.A.; Tsai, S.Y.; Feng, M.; Mundy, G.R.; Harris, S.E.; Hogan, B.L.M.
 J. Biol. Chem. 270, 28364-28373, 1995
 A:Title: The mouse bone morphogenetic protein-4 (BMP4) gene: Analysis of promoter util
 A:Reference number: I49541; MUID:96081880; PMID:7499338
 A:Accession: I49541
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-420 <RES>
 A:Cross-references: GB:I47480; NID:g994733; PIDN:AA037698.1; PID:g994734
 R:Dickinson, M.E.; van der Meer-de Jong, R.; Hogan, B.L.M.
 submitted to the EMBL Data Library, December 1990
 A:Description: Nucleotide sequence of the mouse Bone Morphogenetic Protein-4 (BMP-4)
 A:Reference number: S29523

A:Accession: S29523
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 13-420 <DIC>
 A:Cross-references: EMBL:X56848; NID:g50180; PIDN:CAA40179.1; PID:g50181
 R:Dickinson, M.E.; Kobrin, M.S.; Silan, C.M.; Kingsley, D.M.; Justice, M.J.; Miller, J.; Jenkins, N.A.
 Genomics 6, 505-520, 1990
 A:Title: Chromosomal localization of seven members of the murine TGF-beta superfamily
 A:Reference number: A34201; MUID:90228966; PMID:1970330
 A:Accession: B34201
 A:Status: preliminary
 A:Molecule type: nucleic acid sequence not shown; not compared with conceptual

A49147
bone morphogenetic protein 4 - African clawed frog
N:Alternate names: BMP-4; ventralizing factor
C:Species: *Xenopus laevis* (African clawed frog)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C:Accession: A49147
R:Date, L.: Howes, G.; Price, B.M.; Smith, J.C.
Development 115, 573-585, 1992
A:Title: Bone morphogenetic protein 4: a ventralizing factor in early *Xenopus* development
A:Reference number: A49147; MUID:93048819; PMID:1425340
A:Accession: A49147
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-400 <DAL>
A:Cross-references: GB:X64538; GB:S46999; NID:964559; PIDN:CA45836.1; PIDs:964590
A:Experimental source: XTC cells
A:Note: Sequence extracted from NCBI backbone (NCBIN:117127, NCBIPI:117128)
i:Superfamily: Inhibin

	Query Match	32.9%	Score 326.5;	DB 2;	Length 400;
	Best Local Similarity	23.8%	Pred. 1.8e-20;		
	Matches 78;	Conservative 35;	Mismatches 72;	Indels 53;	Gaps 7;
Oy	29	WETEVSSAYKRWVADSTNNKKLEV----	TYOSHRESCOTLDISVP-----	SGKNIP	79
	11: : : :	11: : : :	11: : : :		
Db	207	WESDVSPALIMRTROKQINHGALIEVILHNOTKTHQCKHVRISRLIPEDADNQMCP			266
Oy	80	FFVYVSDNRBNGCKETRIDLLEKMGHEDEPLXYTANAAQAGSEQSEEGELDTYANG			139
	11:	11:			
Db	267	LLIFSHDGR-----GH-----ALTRSKRS-----			287
Oy	140	PLARRKRSYGASHQCKSTLRVNEFDIDGMSWIIAPREYATYCKKGGCFPLADDTYPI			199
	11:	11:	11:		
Db	288	----PKQDRPKKKKKRRHRSLLVYDSDDGMWMIYALPFGYALFCHQDCCFPPLADHINSG			344
Oy	200	KHALVOTVLHLKPTTVYGAACCVPTKLSPLSITLKKDMGVETLKYHTEGMSVAEGCGR			257
	11:	11:	11:		
Db	345	NHALVOTVLN-SYNASIPKACCPPELSSISMLIADYEDKYALK-NQOEIVAGCCGR			400

RESULT 10
A26158
decentapleptic protein precursor - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C:Date: 24-Jun-1987 #sequence_revision 24-Jun-1987 #text_change 16-Apr-1999
C:Accession: A26158
R:Padgett, R.W.; St. Johnston, R.D.; Gelbart, W.M.
N:ature 325, 81-84, 1987
A:Title: A transcript from a *Drosophila* pattern gene predicts a protein homologous to the
A:Reference number: A26158; MUID:87090408; PMID:3467201
A:Accession: A26158
A:Molecule type: mRNA
A:Residues: 1-588 <PAD>
A:Cross-references: GB:M30116; NID:g157291; PID:g157292
C:Genetics:
A:Gene: flyBase:dpp
A:Cross-references: flyBase:FBgn0000490
A:Keywords: glycoprotein
F:15/Domain: signal sequence #status predicted <SIG>
F:120/342.377.529/Binding site: carbohydrate (Asn) (covalent) #status predicted

```

Query Match      23.8% Score 325; DB 2; Length 588;
Best Local Similarity 30.5%; Pred. No. 3,9e-20;
Matches 92; Conservative 45; Mismatches 115; Indels 50; Gaps 9;

Oy    4 EDSETHQAGCTGTFYASODIR-----DEGWETLEY-----SSAVKRWADSTYNKKKLEY 55
      :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db    289 KDSIKIDRRFHNNHRLPDKVSIPADELKRAEELQLTRDLISQQVAASSSNRRRIYY 348
      :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::

Oy    56 T-----VQSIRE-----SCDTLDISVPG-----SKNLPFFEVES 85
      :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db    349 LVYDITRVVGGRGREGSYLLDITKVTLRNLSTDIVSLAQPVADHWMLASPORNGGLLVEYA 408
      :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::

```

OY	86	NDS-----NGKETRIDLKEMTCHQETMLVUTANKAAVOGAGEEGEEDJGTAV	138
Dd	409	TYSLSLRPAPHHHYRLRRSDAHENRMOHKRPLLFTTTDDGRKK-ARSLRDVSOGGEGGKG	467
OY	139	GPLLARRKRSSTGASSH---CQXTSLRVNFEDIGDMSWIIAPREYDAYECKSGCFPLADD	195
Dd	468	GRNKRHARRBPTRKKNHDTCRRHSLSYDFESVDGMDDIVAPLGYDAYCGHGCPFLADH	527
OY	196	VTPPKAIAIQTULVHLKFPFKYGKACVPPTKLSPILXIKDDMGVPTLKYHEGMSVAECG	255
Dd	528	FNSTNHAAVVOTLVNNMNGKVPKACVPTQLDLSAYMLYLNDOSTVYALK-NYQEMTVVCGG	586
OY	256	CR 257	
Dd	587	CR 588	

```

RESULT 11
JH0688
bone morphogenetic protein 2II precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C:Accession: JH0688
R:Nishimatsu, S.; Suzuki, A.; Shoda, A.; Murakami, K.; Ueno, N.
Biochem Biophys Res Commun 186, 1487-1495, 1992
A:Title: Genes for bone morphogenetic proteins are differentially transcribed in cartilage
A:Reference number: JH0687; MUID:92376016; PMID:1510675
A:Accession: JH0688
A:Molecule type: mRNA
A:Residues: 1,396<MIS>
A:Cross-references: GB:X63425; NID:g64583; PIDN:CAA45019.1; PID:g64584
A:Experimental source: oocyte
C:Superfamily: Inhibin
C:Keywords: glycoprotein
A:ID:285-398/Produce: bone morphogenetic protein 2II #status predicted <MAT>
A:ID:137,202,237,340/Binding site: carboxylate (Asn) (covalent) #status predicted
A:ID:137,202,237,340/Binding site: carboxylate (Asn) (covalent) #status predicted

```

[illegible]

RESULT 12
JH0687
bone morphogenetic protein 21 precursor - African clawed frog
C:Species: *Xenopus laevis* (African clawed frog)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C:Accession: JH0687; S16244
C:RNALocus: S.; Suzuki, A.; Shoda, A.; Murakami, K.; Ueno, N.
Biochem. Biophys. Res. Commun. 186, 1487-1493, 1992
A:Title: Genes for bone morphogenetic proteins are differentially transcribed in early
A:Reference number: JH0687; MUID:92378616; PMID:1510675
A:Accession: JH0687

A:Molecule type: mRNA
A:Residues: 1-398 <NTS>
A:Cross-references: GB:653424; NID:g64585; PIDN:CAA45018.1; PID:g64586
A:Experimental source: oocyte
R:Piessow, S.; Koester, M.; Knoechel, W.
Biochim. Biophys. Acta 1089, 280-282, 1991
A>Title: cDNA sequence of Xenopus laevis bone morphogenetic protein 2 (BMP-2).
A:Reference number: S16244; MUID:91274367; PMID:2054389
A:Accession: S16244
A:Molecule type: mRNA
A:Residues: 1-6,'S','8-15','V',17-232,'N',234-398 <PIE>
A:Cross-references: EMBL:X55031; NID:g64581; PIDN:CAA38850.1; PID:g64582
C:Superfamily: Inhibin
F:Keywords: dimer; glycoprotein
F:285-358/Product: bone morphogenetic protein 2i #status predicted <MAT>
F:137,202,340/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 23.2%; Score 318; DB 2; Length 398;
Best Local Similarity 33.8%; Pred. No. 9,5e-20;
Matches 80; Conservative 29; Mismatches 76; Indels 52; Gaps 7;

OY 29 WETLEVSAAKRWVRADSTTKNKILEVTVOGSHRESCTLDI---SYPPGSKN---LPF 80
||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
DB 206 WESEFVTPALAKWIAHKQPNHGFVEVETHLDNDKNVPKCHVIRISLTLPDDNNPQRIPL 265
|||||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
OY 81 FVFESNDNSNGTKETRLDLLKEMIGHEOETMLVYTAKNAAGAGSGOEELGDGYTAGVP 140
||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
DB 266 LVTFESHDK-----GH-----ALHKRKQKQ----- 285

OY 141 LLARKRSTGAASHCOQTSLNVNFEDIGDMSWTIAPEKYDAIECKGCFFPLADVDYPTK 200
DB 286 --ARRKKRRLLKSSCRRRPLLYVDSVGWMNDMVIAPPGYNAFYCHGECPFLADHLNSTN 343
|||||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
OY 201 HAIVOTLVHKEFTPVGRACCVPTKLSPISILYVDMDMVPLTKLHYEGSMVAECGCR 257
|||||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
DB 344 HAIVOTLVN-SVNTNIPKACCVPELSAISMLYIDENKVVLK-NYQDMVVEGGCR 398
|||||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

RESULT 13
JH0689
bone morphogenetic protein 4 precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C:Accession: JH0689
R:Nishimatsu, S.; Suzuki, A.; Shoda, A.; Murakami, K.; Ueno, N.
Biochem. Biophys. Res. Commun. 186, 1487-1495, 1992
A>Title: Genes for bone morphogenetic proteins are differentially transcribed in early a
A:Reference number: JH0687; MUID:92378616; PMID:1510675
A:Accession: JH0689
A:Molecule type: mRNA
A:Residues: 1-401 <NTS>
A:Cross-references: GI:X63426; NID:g64587; PIDN:CAA45020.1; PID:g64588
A:Experimental source: oocyte
C:Superfamily: inhibin
F:Keywords: glycoprotein
F:288-401/Product: bone morphogenetic protein 4 #status predicted <MAT>
F:141,204,238,343,358/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 23.1%; Score 316.5; DB 2; Length 401;
Best Local Similarity 33.2%; Pred. No. 1.3e-19;
Matches 79; Conservative 31; Mismatches 75; Indels 53; Gaps 7;

OY 29 WETLEVSAAKRWVRADSTTKNKILEV-----TVGSH--RESCDTILDIVPPESKMLP 79
||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
DB 208 WESEFVSPIAKMKWTLDKOINHG LAEVTHLNQTKYQGKHVIRISLTLPORDADWSOMRP 267
|||||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
OY 80 FFVFSVSNRSNGTKETRLDLLKEMIGHEOETMLVYTAKNAAGAGSGOEELGLDGYTAGV 139
|||||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
DB 268 ILITPSHDGR-----GH-----ALVTRSRKS----- 288

OY 140 PLLARKRSTGAASHCOQTSLRVNFEDIGDMSWTIAPEKYDAIECKGCFFPLADVDYPT 199
DB 286 ---PQQQPRKKRNKRHSILYVDSVGWMNDMVIAPPGYDAFYCHGCEPFLADHLNST 345

[illegible]

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OM protein - protein search, using sw model

Run on: April 2, 2003, 14:51:46 ; Search time 36 seconds
(without alignments)

436.443 Million cell updates/sec

Title: US-10-002-278-9

Sequence: 1 DVLDESETWQATGTCTFLV.....GVPFLKHYEGMSVAECGR 257

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 248812 segs, 61136040 residues

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

Published Applications_AAI*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCRT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/PCRTUS_PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1368	100.0	257	12	US-10-002-278-9 Sequence 9, Appl1
2	808.5	59.1	427	12	US-10-002-278-2 Sequence 2, Appl1
3	516.5	37.8	425	9	US-09-813-398-32 Sequence 32, Appl1
4	361	26.4	419	10	US-09-784-911-2 Sequence 2, Appl1
5	354	25.9	437	10	US-09-784-911-4 Sequence 4, Appl1
6	350	25.6	427	10	US-09-784-911-6 Sequence 6, Appl1
7	349.5	25.5	421	9	US-09-945-182-26 Sequence 26, Appl1
8	345	25.2	408	9	US-09-804-625-6 Sequence 6, Appl1
9	345	25.2	409	10	US-09-749-728B-69 Sequence 69, Appl1
10	345	25.2	409	9	US-09-813-398-27 Sequence 27, Appl1
11	337.5	24.7	263	9	US-09-945-182-32 Sequence 32, Appl1
12	334.5	24.5	411	9	US-09-945-182-28 Sequence 28, Appl1
13	330	24.1	436	10	US-09-730-772-14 Sequence 14, Appl1
14	330	24.1	436	10	US-09-735-849-14 Sequence 14, Appl1
15	322	23.5	451	10	US-09-784-911-10 Sequence 10, Appl1
16	320	23.4	433	10	US-09-784-911-8 Sequence 8, Appl1
17	313	22.9	433	10	US-09-784-911-12 Sequence 12, Appl1
18	312.5	22.8	455	9	US-09-813-398-28 Sequence 28, Appl1
19	312	22.8	435	10	US-09-784-911-14 Sequence 14, Appl1

20	311	22.7	396	9	US-10-044-716-2 Sequence 2, Appl1
21	311	22.7	396	10	US-09-804-625-4 Sequence 4, Appl1
22	311	22.7	396	10	US-09-952-360-2 Sequence 2, Appl1
23	311	22.7	397	9	US-09-813-398-24 Sequence 24, Appl1
24	310	22.7	118	12	US-10-115-406-15 Sequence 15, Appl1
25	310	22.7	143	12	US-10-002-278-4 Sequence 4, Appl1
26	308	22.5	502	9	US-09-813-398-37 Sequence 37, Appl1
27	307	22.4	501	8	US-08-981-480B-1 Sequence 1, Appl1
28	306	22.4	501	10	US-09-730-772-13 Sequence 13, Appl1
29	306	22.4	501	10	US-09-735-849-13 Sequence 13, Appl1
30	305.5	22.3	431	8	US-08-822-186-2 Sequence 2, Appl1
31	305.5	22.3	431	8	US-08-937-755-2 Sequence 2, Appl1
32	305.5	22.3	431	9	US-09-982-543A-10 Sequence 10, Appl1
33	305.5	22.3	431	9	US-10-062-370-5 Sequence 5, Appl1
34	305.5	22.3	431	9	US-09-039-107-2 Sequence 2, Appl1
35	305.5	22.3	431	9	US-09-798-518-1 Sequence 1, Appl1
36	305.5	22.3	431	10	US-09-045-331-2 Sequence 2, Appl1
37	305.5	22.3	431	10	US-09-828-607-2 Sequence 2, Appl1
38	305.5	22.3	432	9	US-10-270-377-3 Sequence 3, Appl1
39	305.5	22.3	432	10	US-09-361-741-3 Sequence 3, Appl1
40	305.5	22.3	495	9	US-09-880-708-10 Sequence 10, Appl1
41	304	22.2	294	9	US-09-945-182-2 Sequence 2, Appl1
42	304	22.2	388	9	US-09-945-182-34 Sequence 34, Appl1
43	302.5	22.1	119	8	US-08-945-459A-1 Sequence 1, Appl1
44	302.5	22.1	119	9	US-09-068-253-2 Sequence 2, Appl1
45	302.5	22.1	120	9	US-09-945-182-4 Sequence 4, Appl1

ALIGNMENTS

RESULT 1

US-10-002-278-9
Sequence 9, Application US/10002278
Patent No. US2002013234A1
GENERAL INFORMATION:
APPLICANT: Janssen, Thomas M.
APPLICANT: Janssen, Thomas M.
APPLICANT: Janssen, Thomas M.
TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF DORSALIN-1
FILE REFERENCE: 0575/40314-A
CURRENT APPLICATION NUMBER: US-10/002,278
CURRENT FILING DATE: 2001-11-02
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 257
TYPE: PRT
ORGANISM: Mouse
US-10-002-278-9

Query Match	100.0%	Score 1368	DB 12	Length 257
Best Local Similarity	100.0%	Pred. No. 2.2e-128		
Matches 257	Conservative 0	Mismatches 0	Indels 0	Gaps 0
1	DVLDESETWQATGTCTFLV	SODIRDEGNETLEVS	AVYRWVRADSTNNKKLEVTQSH	60
1	DVLDESETWQATGTCTFLV	SODIRDEGNETLEVS	AVYRWVRADSTNNKKLEVTQSH	60
61	RESCDTLDISVPPGSKLP	FEVVFSSNDKSNKRETRDL	LKMTICHEDETMUYTKAKNAY	120
61	RESCDTLDISVPPGSKLP	FEVVFSSNDKSNKRETRDL	LKMTICHEDETMUYTKAKNAY	120
61	RESCDTLDISVPPGSKLP	FEVVFSSNDKSNKRETRDL	LKMTICHEDETMUYTKAKNAY	120
121	OGAGESEEBEGIDYTV	AGPLARRRSTGASHCOKT	SLRVNFEIDIMDSMIITAPREYD	180
121	OGAGESEEBEGIDYTV	AGPLARRRSTGASHCOKT	SLRVNFEIDIMDSMIITAPREYD	180
121	OGAGESEEBEGIDYTV	AGPLARRRSTGASHCOKT	SLRVNFEIDIMDSMIITAPREYD	180
181	AYEKKGCGFPPLADVT	PTTHAIVQVLVHLKPTTKV	GRACCPYTKLSITLYKDDMGVP	240
181	AYEKKGCGFPPLADVT	PTTHAIVQVLVHLKPTTKV	GRACCPYTKLSITLYKDDMGVP	240
241	TLKRYHEGMSVAECGR	257		


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Db      61 LLLDARTLDPGAPBAGWEVFDWQGLRHQPMKQLCLPLRAA---WGELDA---GEMEA 113
Qy      56 TVOSHRESCDTLDSVPGSKNLPF-----FVFSNDNSNGTKETRLDLKEM 103
Db      114 RARGPOQ-----PPPDRLRSIGFGRVRPPQERALLVVF-----TRSQKMLFEM 159
Qy      104 IGHQETMLVTKANAYAGSGESGEEGLDGYTAVGPLY-----ARRKSTGASH----- 154
Db      160 ---REQ---LGSAAAGAGAGAGSGSWPPPSGAPDARPMWLPSCGRRRRTAFASRHGRHG 213
Qy      155 -----CQKTLRVNFDIGDMSWITAPKREYDAYECKGCGFPPLADDTPTKHAIVOTLV 208
Db      214 KKSRLRCKKPLHVNFKELMDWDITAPLETFEYHCEGVCDPFLSHLEPTNHAIQPLM 273
Qy      209 HLKPTFKVACVPTKLSPTSLYKDDMGVPTLKHYHSGMSVAGCGCR 257
Db      274 NSMDGSPSPSCVPTKLTPLISILY-IDAGNNVYKQYEDMNVESGCCR 321

```

RESULT 8

```

US-09-804-625-6
; Sequence 6, Application US/09804625
; Publication No. US20030049826A1
; GENERAL INFORMATION:
;   APPLICANT: Wang, Elizabeth A.
;               Rosen, Vicki A.
;               Wozney, John M.
; TITLE OF INVENTION: NO. US20030049826A1el BMP Products
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: LEGAL AFFAIRS, GENETICS INSTITUTE, INC.
;   STREET: 87 CAMBRIDGE PARK DRIVE
;   CITY: CAMBRIDGE
;   STATE: MA
;   COUNTRY: USA
;   ZIP: 02140
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/804,625
;   FILING DATE: 09-Mar-2001
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/925,779
;   FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
;   NAME: Kapinos, Ellen J.
;   REGISTRATION NUMBER: 32,245
;   REFERENCE/DOCKET NUMBER: 5160C
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 617-876-1170
;   TELEFAX: 617-876-5851
; INFORMATION FOR SEQ ID NO: 6:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 408 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;     MOLECULE TYPE: protein
;   SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-804-625-6

```

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Query Match      25.2%; Score 345; DB 9; Length 408;
Best Local Similarity 35.9%; Pred. No. 3.3e-26;
Matches 85; Conservative 28; Mismatches 76; Indels 48; Gaps 7;

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Qy      29 WETLEVSAYVRWVRADSTINKKLEYT-----VQSHRESCDTLDSVPGSKN---LPF 80
Db      212 WETFDVSPAVLMTREKOPNYGLAIEVTHLQTRHOGOHVRSLSLPQSGNMAQLRPL 271

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```

Qy      81 FVFSNDNSNGTKETRLDLKEMIGHQETMLVTKANAYAGSGESGEEGLDGYTAVGP 140
Db      272 LVTFGHD-GRGHALTTRRRRAKSPKHSQR----- 300
Qy      141 ILARRKSTGASSHCQKTSIRVNFEDIGDMSWITAPKEYDAYECKGCGFPPLADDTPTK 200
Db      301 ---ARKK-----NKNCRRHSILYVDFSDVGMNDWIVAPGYOAFCHGDCFPPLADHINSTN 353
Qy      201 HAIVOTLVHLKPTFKVACVPTKLSPTSLYKDDMGVPTLKHYHSGMSVAGCGCR 257
Db      354 HAIVOTLVN-SVNSSIRACCVPTELSISMILYLDYEDVVLK-NIQENMVAGCGCR 408

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RESULT 9

```

US-09-749-728B-69
; Sequence 69, Application US/09749728B
; Patent No. US20020142457A1
; GENERAL INFORMATION:
;   APPLICANT: Umezawa, Akihito
;   APPLICANT: Hata, Jun-ichi
;   APPLICANT: Fukuda, Keiichi
;   APPLICANT: Ogawa, Satoshi
;   APPLICANT: Sakurada, Kazuhiko
;   APPLICANT: Gojo, Satoshi
;   APPLICANT: Yamada, Yoji
; TITLE OF INVENTION: THE CELL HAVING THE POTENTIALITY OF DIFFERENTIATION INTO CARDI
; FILE REFERENCE: 00766.000043
; CURRENT APPLICATION NUMBER: US/09/749,728B
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 2001-09-17
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: PCT-JP00-01148
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: PCT-JP00-07741
; PRIOR FILING DATE: 2000-11-02
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn Ver.2.0
; SEQ ID NO 69
; LENGTH: 408
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-749-728B-69

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```

Query Match      25.2%; Score 345; DB 10; Length 408;
Best Local Similarity 35.9%; Pred. No. 3.3e-26;
Matches 85; Conservative 28; Mismatches 76; Indels 48; Gaps 7;

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Qy      29 WETLEVSAYVRWVRADSTINKKLEYT-----VQSHRESCDTLDSVPGSKN---LPF 80
Db      212 WETFDVSPAVLMTREKOPNYGLAIEVTHLQTRHOGOHVRSLSLPQSGNMAQLRPL 271
Qy      81 FVFSNDNSNGTKETRLDLKEMIGHQETMLVTKANAYAGSGESGEEGLDGYTAVGP 140
Db      272 LVTFGHD-GRGHALTTRRRRAKSPKHSQR----- 300
Qy      141 ILARRKSTGASSHCQKTSIRVNFEDIGDMSWITAPKEYDAYECKGCGFPPLADDTPTK 200
Db      301 ---ARKK-----NKNCRRHSILYVDFSDVGMNDWIVAPGYOAFCHGDCFPPLADHINSTN 353
Qy      201 HAIVOTLVHLKPTFKVACVPTKLSPTSLYKDDMGVPTLKHYHSGMSVAGCGCR 257
Db      354 HAIVOTLVN-SVNSSIRACCVPTELSISMILYLDYEDVVLK-NIQENMVAGCGCR 408

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RESULT 10

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US-09-813-398-27
; Sequence 27, Application US/09813398
; Patent No. US20020169292A1
; GENERAL INFORMATION:
;   APPLICANT: Bruce D. Weintraub
;   APPLICANT: Mariusz W. Szkulinski
;   APPLICANT: University of Maryland
; TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS

```

1 APPLICATION NUMBER: 08/808,324
2 FILING DATE: <Unknown>
3 ATTORNEY/AGENT INFORMATION:
4 NAME: Lazar, Steven R
5 REGISTRATION NUMBER: 32,618
6 REFERENCE/DOCKET NUMBER: 5202-D
7 TELECOMMUNICATION INFORMATION:

Job time : 37 secs

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-735-849-14

Query Match 24.1%; Score 330; DB 10; Length 436;
Best Local Similarity 36.7%; Pred. No. 1.1e-24;
Matches 81; Conservative 23; Mismatches 67; Indels 50; Gaps 7;

QY 72 PRGSKNLPF-----FVPSNDSNGKTRDLKEMIGHQETMLYKTAKNA 119
DB 231 PPDLSRLGFGRRVTPQERALLVFSRSQ---RKLFAEMREDLGSATEVY----- 278
QY 120 YGAGESQEEEG-----LDGYTAVG---PLARRKSTGASSH-----CQ 156
DB 279 --GPGGGAEGSGPPPPPPPPGTPDAGLWSPSPCRRRRRTAFASRHGKRHKKSRLRCS 336
QY 157 KTSLRVNEFDIGDMSWLIARKEVDAYECKGCEFFPLADDVPTTKHAIYOTLVHLKFPYKV 216
DB 337 KKPLHVNFKELGMDWMIILAPLEYAYHCEGVCDPFLRSHLEPTNHAIIOTLMNSMDPGST 396
QY 217 GKACCVPTKLSPIISILYKDDMGVPTLKYHYESMSVAECGR 257
DB 397 PPSCCVPTKLTPLPSILY-IDAGNNVYVNEEEMVYESGCCR 436

RESULT 15

US-09-784-911-10
; Sequence 10, Application US/09784911
; Patent No. US20020072115A1
; GENERAL INFORMATION:
; APPLICANT: Harrison, Leonard C.
; APPLICANT: Jiang, Fang-Xu
; APPLICANT: Stanley, Edouard Guy
; APPLICANT: Gomez, Leonel Jorge
; TITLE OF INVENTION: Pancreatic islet cell growth factors
; FILE REFERENCE: Davies Collison Cave
; CURRENT APPLICATION NUMBER: US/09/784, 911
; CURRENT FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent version 2.1
; SEQ ID NO 10
; LENGTH: 451
; TYPE: PRT
; ORGANISM: mouse
US-09-784-911-10

Query Match 23.5%; Score 322; DB 10; Length 451;

Best Local Similarity 32.9%; Pred. No. 7.3e-24;
Matches 93; Conservative 35; Mismatches 91; Indels 64; Gaps 12;

QY 5 DSETW-----DQATGKTFLVSODIR----DEGWETLEVSAVKRWVRADSTKN 51
DB 185 DNEFFQITVYOVLOEHSGRESDFLDSRTIMASEGWLVPDITATSNHWV---VNPRH 240
QY 52 KLEVYVQSHRESCDTLD-ISVPP-----GSKN-LPFFVVFSDNSNGKTRDLDL 100
DB 241 NLGQL-----SVETLDGQSINPKLGLGRHGPQKPPMFAFK-----ATEVHLRSI 290
QY 101 KEMIGHQETMLYK-----TAKMAVQAGASQEEEGLDGTAVGPLLARRKSTGASS 153
DB 291 RSTGTRQEOELISEEDLJRTQSDVSRSG--SSDYNSELKTA----- 333
QY 154 HCOKTSLRVNEFDIGDMSWLIARKEVDAYECKGCEFFPLADDVPTTKHAIYOTLVHLKFP 213
DB 334 -CKKHLYVSRQDLGMDWMIILAPKGYAANCQEGECSEFPLNHNATNHAIIYOTLVHLNMP 392
QY 214 TKVGKACCVPTKLSPIISILYKDDMGVPTLKYHYESMSVAECGC 256
DB 393 EYVPRCCAPTKLNAISLYFDNDSNVTLK-KYRNMYVRACGC 434

Search completed: April 2, 2003, 15:00:43

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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 2, 2003, 14:40:05 : Search time 75 seconds
(Without alignments)
456.605 Million cell updates/sec

Title: US-10-002-278-9
Perfect score: 1368
Sequence: 1 DYLEDSETWQATGKTKFLV.....GVPTLKHYEGHVAECGR 257

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: /SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
- 2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
- 3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
- 4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
- 5: /SID52/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
- 6: /SID52/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
- 7: /SID52/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
- 8: /SID52/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
- 9: /SID52/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
- 10: /SID52/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
- 11: /SID52/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
- 12: /SID52/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
- 13: /SID52/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
- 14: /SID52/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
- 15: /SID52/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
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- 20: /SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
- 21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
- 23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1336.5	97.7	428	AA1372	Murine bone morpho
2	1336.5	97.7	428	AA1372	Murine bone morpho
3	1336.5	97.7	428	AA1372	Murine bone morpho
4	1146.5	83.8	429	AA12410	Albunin fusion pro
5	1146.5	83.8	429	AA14195	Human novel protei
6	1146.5	83.8	429	AA14195	Human novel protei
7	808.5	59.1	16	AA14195	Dorsalin I, Galili
8	634	46.3	150	AA186903	Human BMP-9 polype
9	634	46.3	150	AA186903	Human bone morphog
10	619	45.2	150	AA1374	Human bone morphog

11	506	43.6	110	23	AA1930	Human TGFbeta prot
12	519.5	38.0	312	16	AA16200	Part of Dvovine bon
13	516.5	37.8	424	21	AA16202	Complete human bon
14	516.5	37.8	424	21	AA16202	Human bone morphog
15	508	37.1	421	20	AA16304	Mouse pancreatic-d
16	469	34.3	103	20	AA16715	Mouse pancreatic-d
17	469	34.3	103	21	AA16715	Chicken Dorsalin,
18	469	34.3	103	21	AA16715	Chicken Dorsalin,
19	469	34.3	103	21	AA16715	Chicken Dorsalin,
20	400.5	29.3	393	20	AA192568	Dorsalin finger-1
21	384.5	28.1	108	22	AA16302	Mouse pancreatic-d
22	361	26.4	419	22	AA151926	Human TGFbeta prot
23	354	25.9	437	22	AA166568	BMP 4/4 glu polype
24	350	25.6	427	22	AA166569	BMP 4/6 glu polype
25	349.5	25.5	427	22	AA166570	BMP 4/6 myc polype
26	349.5	25.5	321	18	AA18730	Human mature VL-1
27	349.5	25.5	321	18	AA18730	Human bone morphog
28	349.5	25.5	321	18	AA18730	Human bone morphog
29	349.5	25.5	321	18	AA18730	Human bone morphog
30	349.5	25.5	321	18	AA18730	Human bone morphog
31	348.5	25.5	417	16	AA17604	Human growth/diffe
32	345	25.2	408	9	AA179476	Human extracellular
33	345	25.2	408	12	AA180620	Mouse BMP-4, Mus
34	345	25.2	408	12	AA180620	Human bone morphog
35	345	25.2	408	12	AA180620	Human BMP-2B in la
36	345	25.2	408	14	AA14748	Osteogenic protein
37	345	25.2	408	14	AA13735	Human bone morphog
38	345	25.2	408	15	AA13735	Human BMP-4, Homo
39	345	25.2	408	15	AA13735	Prepro human CBMP2
40	345	25.2	408	17	AA185761	Human CBMP2B, Hom
41	345	25.2	408	17	AA185761	Human BMP-4, Homo
42	345	25.2	408	18	AA124850	Human bone morphog
43	345	25.2	408	18	AA124850	Human BMP-2B, Hom
44	345	25.2	408	19	AA143104	Human osteogenic p
45	345	25.2	408	20	AA143112	Human prepro CBMP2
					AA189681	Human osteogenic p

ALIGNMENTS

RESULT 1	
ID	AA1372
AA1372	standard; Protein; 428 AA.
AC	AA1372:
XX	
XX	24-JUN-1993 (first entry)
DE	Murine bone morphogenic protein-9 (BMP-9).
XX	
KW	bone formation; cartilage formation; wound healing; tissue repair;
KW	surgery; fracture treatment; periodontal disease; osteoporosis;
KW	increase neuronal survival; transplantation; nerves; nervous system.
XX	
OS	Mus musculus.
FX	
FT	Key
FT	Protein
XX	
XX	Location/Qualifiers
XX	319..427
XX	/label= mature peptide
XX	
XX	WO930432-A.
XX	
XX	07-JAN-1993.
XX	
XX	25-JUN-1992; 92WO-US05374.
XX	
XX	25-JUN-1991; 91US-0720590.
XX	
XX	(GENY) GENETICS INST INC.
XX	
XX	Celeste AJ, Wozney JM;
XX	
XX	WPL; 1993-036379/04.

DR N-PSDB; AA035243.

XX New BMP-9 polypeptide(s) induce bone and cartilage formation -
PT used for treating osteoporosis and fractures, healing wounds and
PR increasing neuronal survival

XX Claim 1; Fig 1; 60pp; English.

XX This sequence is thought to be the primary translation product of
CC murine bone morphogenetic protein. Based on the knowledge of other
CC BMP's and proteins within the TGF-beta family it is predicted that
CC the precursor polypeptide would be cleaved at the multibasic
CC sequence Arg-Arg-Lys-Arg. In agreement with the proposed consensus
CC proteolytic processing sequence of Arg-X-X-Arg to generate a 110
CC amino acid mature peptide. It is expected that processing into the
CC mature form will involve dimerisation and removal of the N-terminal
CC region in a manner analogous to the related protein TGF-beta,
CC giving a homodimer of 2 subunits each with a molecular weight of
CC approx. 12,000 Da. The protein can be used to induce bone and/or
CC cartilage formation and in wound healing and tissue repair. It
CC can be used in surgery of the treatment of fractures, periodontal
CC disease or osteoporosis. The protein can also increase neuronal
CC survival and can be used in transplantation and treatment of
CC conditions exhibiting a decrease in neuronal survival.

CC Sequence 428 AA;

SO Query Match 97.7%; Score 1336.5; DB 14; Length 428;

Best Local Similarity 98.4%; Pred. No. 9,9e-129; Mismatches 1; Gaps 1;

Matches 253; Conservative 2; Indels 1;

OY 1 DVLDESEMTDQATGKTFFLVSDIRDEGWETLEVSAAVRRWRADSTNNKLEVTYQSH 60
DB 173 DVLDESEMTDQATGKTFFLVSDIRDEGWETLEVSAAVRRWRADSTNNKLEVTYQSH 232

OY 61 RESCDTLDISVPSSKMLPFYVFSNDRSNGTETRLDLKEMIGHDETMLVTKAKAY 120
DB 233 RESCDTLDISVPSSKMLPFYVFSNDRSNGTETRLDLKEMIGHDETMLVTKAKAY 291

OY 121 QGAGESQEEGLDGYTAVGPLLARRKSTGASSHCOKTSLRVNFDIGDMSWIIAPKEYD 180
DB 292 QGAGESQEEGLDGYTAVGPLLARRKSTGASSHCOKTSLRVNFDIGDMSWIIAPKEYD 351

OY 181 AYECKGGCFPLADVPPTKHAIVQTLVHLKFTKVGKACVPTKLSPISTILYKDDMGVP 240
DB 352 AYECKGGCFPLADVPPTKHAIVQTLVHLKFTKVGKACVPTKLSPISTILYKDDMGVP 411

OY 241 TLKHYEGMSVAECGCR 257
DB 412 TLKHYEGMSVAECGCR 428

RESULT 2

ID AAR86905 standard; Protein; 428 AA.

AC AAR86905;

DT 10-MAY-1996 (first entry)

DE Murine BMP-9.

KW BMP-9; bone; cartilage; wound healing; liver; tissue repair.

OS Mus musculus strain C57B6xCBA.

XX Key Location/Qualifiers

FT Cleavage-site 318..319

FT Protein /note="proteolytic cleavage site"

PN M09533830-A1.

XX 14-DEC-1995.

XX 05-JUN-1995; 95MO-US07084.

XX 06-JUN-1994; 94US-0254353.

XX (GENE) GENETICS INST INC.

XX Celeste AJ, Rosen VA, Song JJ, Thies SR, Wozney JM;

XX WPI: 1996-040235/04.

XX N-PSDB; AA074084.

XX BMP-9 protein able to induce bone and cartilage formation - also
PT useful in wound healing, tissue repair and for inducing hepatic
PR growth and function

XX Example 1; Page 36-38; 75pp; English.

XX Murine BMP-9 protein (AAR86905) is the product of a cDNA clone,
CC ML14 (AA074084), isolated from a mouse liver cDNA library. The
CC primary translation product is cleaved to yield a 110-amino acid
CC protein that forms a mature, homodimeric, active species.

CC Recombinant BMP-9 is obtd. by expression of the cDNA in procarlyotic
CC or eucaryotic hosts. It has therapeutic applns. in the
CC formation of bone and cartilage, wound healing and tissue repair.

CC Sequence 428 AA;

SO Query Match 97.7%; Score 1336.5; DB 17; Length 428;

Best Local Similarity 98.4%; Pred. No. 9,9e-129; Mismatches 1; Gaps 1;

Matches 253; Conservative 2; Indels 1;

OY 1 DVLDESEMTDQATGKTFFLVSDIRDEGWETLEVSAAVRRWRADSTNNKLEVTYQSH 60
DB 173 DVLDESEMTDQATGKTFFLVSDIRDEGWETLEVSAAVRRWRADSTNNKLEVTYQSH 232

OY 61 RESCDTLDISVPSSKMLPFYVFSNDRSNGTETRLDLKEMIGHDETMLVTKAKAY 120
DB 233 RESCDTLDISVPSSKMLPFYVFSNDRSNGTETRLDLKEMIGHDETMLVTKAKAY 291

OY 121 QGAGESQEEGLDGYTAVGPLLARRKSTGASSHCOKTSLRVNFDIGDMSWIIAPKEYD 180
DB 292 QGAGESQEEGLDGYTAVGPLLARRKSTGASSHCOKTSLRVNFDIGDMSWIIAPKEYD 351

OY 181 AYECKGGCFPLADVPPTKHAIVQTLVHLKFTKVGKACVPTKLSPISTILYKDDMGVP 240
DB 352 AYECKGGCFPLADVPPTKHAIVQTLVHLKFTKVGKACVPTKLSPISTILYKDDMGVP 411

OY 241 TLKHYEGMSVAECGCR 257
DB 412 TLKHYEGMSVAECGCR 428

RESULT 3

ID AAY82271 standard; Protein; 428 AA.

AC AAY82271;

DT 16-JUN-2000 (first entry)

DE Murine bone morphogenetic protein 9 SEQ ID NO:2.

KW Bone morphogenetic protein 9; BMP-9; bone defect; cartilage defect;
KW wound healing; tissue repair; hepatic growth; antiliferility;
KW osteopathic; antilarthritic; vulnary.

XX Mus musculus.

XX Key Location/Qualifiers

FT Peptide 1..318

FT Peptide 1..318

PN M09533830-A1.

FT /label= Signal
 FT Protein 319..428
 FT /label= Bone_morphogenetic_c-protein-9
 XX US6034062-A.
 XX 07-MAR-2000.
 XX
 XX 13-MAR-1997; 97US-0815652.
 XX
 XX 13-MAR-1997; 97US-0815652.
 XX
 XX (GEMV) GENETICS INST INC.
 XX
 XX Thies RS, Song JI;
 XX
 XX WPI: 2000-255707/22.
 XX N-PSDB; AA285746.
 XX
 XX Novel bone-morphogenetic protein (BMP)-9 polypeptides, useful in the
 PT treatment of bone and cartilage defects and in wound healing and tissue
 PT repair, as well as hepatic growth and function -
 XX
 XX Claim 1; Column 33-36; 36pp; English.
 XX
 CC A method has been developed for decreasing proliferation of kidney or
 CC lung epithelial cells, or for inhibiting kidney tubule formation, in a
 CC patient. The method comprises administering an amount of a bone
 CC morphogenetic protein 9 (BMP-9) protein. BMP-9 polypeptides from the
 CC invention may be used to induce bone and cartilage formation or other
 CC connective tissue formation, in periodontal disease, in wound healing
 CC and tissue repair, hepatic growth and function, and in regulating lung
 CC and kidney cell function. The polypeptides can be used for healing of
 CC bone fractures, open fracture reduction, improved fixation of artificial
 CC joints, tooth repair processes, treatment of osteoporosis and
 CC osteoarthritis, and as a dietary supplement or as a component of cell
 CC culture media. BMP-9 may also be used for repair and regenerative of
 CC liver cells. The BMP-9 polypeptides may also have angiogenic,
 CC chemotactic and/or chemotactant properties, and may induce collagen
 CC synthesis, fibrosis, differentiation processes, cell proliferative
 CC responses, cell adhesion responses, and migration. When dimerized, the
 CC BMP-9 polypeptide is expected to demonstrate effects on the production
 CC of follicle stimulating hormone (FSH), and so may be used as a
 CC contraceptive, as a fertility inducing therapeutic, and for advancing
 CC the onset of fertility in sexually immature mammals, so as to increase
 CC the lifetime reproductive performance of domestic animals. The present
 CC sequence represents murine BMP-9.
 CC
 XX
 XX
 XX Sequence 428 AA:
 SQ
 Query Match 97.7%; Score 1336.5; DB 21; Length 428;
 Best Local Similarity 98.4%; Pred. No. 9.9e-129;
 Matches 253; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
 QY 1 DVLDSSTMQAATGTFKFLVSODIRDEGWTLEVSAAVRRVADSTNNKLEVTYQSH 60
 Db 173 DVLDSSTMQAATGTFKFLVSODIRDEGWTLEVSAAVRRVADSTNNKLEVTYQSH 222
 QY 61 RESCDTIDISVPPGSKNLPFFVFSNDKRSNGKTRRLDLEMGHDETMVLVTANAY 120
 Db 233 RESCDTIDISVPPGSKNLPFFVFSNDKRSNGKTRRLDLEMGHDETMVLVTANAY 291
 QY 121 QGAESEQEEGLDGYTAGVGPLARRKSTGASSHCOKTSLVNFEIDIGMSIAPREYD 180
 Db 292 QGAESEQEEGLDGYTAGVGPLARRKSTGASSHCOKTSLVNFEIDIGMSIAPREYD 351
 QY 181 AYECKGGCFEPLADDDYTPPKHAIYQTVLHAKRPTKVGAACVPTKLSISILYKDDMGVP 240
 Db 352 AYECKGGCFEPLADDDYTPPKHAIYQTVLHAKRPTKVGAACVPTKLSISILYKDDMGVP 411
 QY 241 TLKHYEGMSVAECGR 257
 Db 412 TLKHYEGMSVAECGR 428

RESULT 4
 ID AE12410
 XX AE12410 standard; Protein; 429 AA.
 XX
 XX AE12410;
 AC
 XX
 XX 18-DEC-2001 (first entry)
 DE
 XX
 XX Albumin fusion protein related human protein #1.
 KW Human; albumin; HA; immune system disorder; transplant rejection;
 KW blood related disorder; myocardial infarction; glomerulonephritis;
 KW hyperproliferative disorder; childhood acute myeloid leukemia;
 KW renal cell carcinoma; cardiovascular disorder; vulvovaginitis; melanoma;
 KW arthralgia; respiratory disorder; non-allergic rhinitis; antileukemic;
 KW neurological disease; Alzheimer's disease; endocrine disorder; measles;
 KW pheochromocytoma; reproductive system disorder; neuroprotective; syphilis;
 KW infectious disease; gastrointestinal disorder; wound healing; neotrophic;
 KW irritable bowel syndrome; HIV; human immunodeficiency virus infection;
 KW cytostatic; antiinflammatory; gene therapy; immunosuppressive; cardiac;
 KW antiarthritic; antineumatic; renal disorder; antimicrobial.
 XX
 XX Homo sapiens.
 OS
 XX
 XX MO200179480-A1.
 PN
 XX
 XX 25-OCT-2001.
 PD
 XX
 XX 12-APR-2001; 2001MO-US11991.
 PF
 XX
 XX 12-APR-2000; 2000US-229358P.
 PR 12-APR-2000; 2000US-199384P.
 PR 21-DEC-2000; 2000US-256931P.
 PR
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX
 XX Rosen CA, Haseltine WA;
 PI
 XX
 XX WPI: 2001-616756/71.
 DR
 XX
 XX Albumin fusion proteins comprising a therapeutic protein and albumin,
 PT useful in the treating metastatic renal cell carcinoma, metastatic
 PT melanoma, malignant melanoma, renal cell carcinoma, HIV (human
 PT immunodeficiency virus) or infection -
 PT
 XX
 XX Disclosure; Page 385-386; 394pp; English.
 PS
 XX
 XX The invention relates to human albumin (HA) fusion proteins and their
 CC corresponding nucleic acid sequences. Therapeutic proteins fused to
 CC albumin or its fragments have an extended shelf-life. The albumin
 CC fusion proteins are useful in the treatment, prevention, diagnosis,
 CC and/or detection of diseases, disorders such as immune system
 CC disorders (e.g. transplant rejection), blood related disorders (e.g.
 CC myocardial infarction), hyperproliferative disorders (e.g. childhood
 CC acute myeloid leukemia, metastatic renal cell carcinoma, metastatic
 CC melanoma, malignant melanoma, renal cell carcinoma), renal disorders
 CC (e.g. glomerulonephritis), cardiovascular disorders (e.g. arthralgias),
 CC respiratory disorders (e.g. non-allergic rhinitis), neurological
 CC diseases (e.g. Alzheimer's disease), endocrine disorders (e.g.
 CC pheochromocytoma), reproductive system disorders (e.g. syphilis),
 CC infectious diseases (e.g. measles), gastrointestinal disorders (e.g.
 CC irritable bowel syndrome), HIV (human immunodeficiency virus) infection
 CC and wound healing. Nucleic acids encoding albumin fusion protein is
 CC used in gene therapy. The present sequence is a human protein related
 CC to albumin fusion proteins.
 CC
 XX
 XX Sequence 429 AA:
 SQ
 Query Match 83.8%; Score 1146.5; DB 22; Length 429;
 Best Local Similarity 82.9%; Pred. No. 3.6e-109;
 Matches 213; Conservative 19; Mismatches 24; Indels 1; Gaps 1;

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QY 1 DVLDESEFWDOATGKTFTPLVSODIRDEGMETLEVSNAVKRMWRADSTTKNKLLEYTVQSH 60
DB 174 DVLDDTDAMDATETKFTPLVSODIRDEGMETLEVSNAVKRMWRADSTTKNKLLEYTVQSH 233
QY 61 RESCDTLDISVPPGSKNLPFFVFNDSNGTETKTRDLKEMIGHEOTMLVKTAKNAY 120
DB 234 RKGCDTLDISVPPGSRNLPFFVFNDSNGTETKTRLE-LREMISHEDQSVLTKLSKOGS 292
QY 121 OGAGSEGEELDGYTAVGPIPLARRKSTGASHCQKTSLRVNFEDIGDMSWIIAPKEYD 180
DB 293 TEAGSSHEEDTDGHVAAGSTLARRKRSAGASHCQKTSLRVNFEDIGDMSWIIAPKEYE 352
QY 181 AVECGGCFEPLADDPVPTKHAIVQTLVHLKFTPKYKACCVPTKLSPIISLYKDDMGVP 240
DB 353 AVECGGCFEPLADDPVPTKHAIVQTLVHLKFTPKYKACCVPTKLSPIISLYKDDMGVP 412
QY 241 TLKYHEGMSVAECGCR 257
DB 413 TLKYHEGMSVAECGCR 429

RESULT 5
AAU14195
AAU14195 standard; Protein: 429 AA.
XX
AC AAU14195;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human novel protein #66.
XX
KW Human; novel protein; Antinaemic; osteopathic; antiinflammatory;
KW immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic;
KW anticonvulsant; antiallergic; cerebroprotective; antifungal; antiviral;
KW antibacterial; antiallergic; dermatological; haemostatic; antistimatic;
KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW tissue regeneration; immune disorder.
XX
OS Homo sapiens.
XX
PN WO20015437-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US02623.
XX
PR 25-JAN-2000; 2000US-0491404.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI: 2001-451939/48.
XX
DR N-PSDB: AAS22500.
XX
PT Isolated polypeptides useful for treating anti-inflammatory diseases,
XX
PT nervous system disorders, and for regenerating bone and cartilage -
XX
PS Example 4: Page 561-562; 894pp; English.
XX
CC The invention relates to polynucleotides encoding novel human
CC proteins or their active domains. The polypeptides, polynucleotides and
CC antibodies raised against the polypeptides are used in a method of
CC treatment of a mammal and prevention of disorders caused by the aberrant
CC protein expression or activity. The polypeptides can be used as
CC molecular weight markers, food supplements, and in antibody production.
CC The polypeptides are used to identify compounds which bind to the
CC polypeptides. Polynucleotides of the invention are used as probes and
CC primers, for sequencing, for chromosome or gene mapping, in the
CC production of recombinant proteins, and in generating anti-sense DNA or
CC RNA and in gene therapy. Polypeptides of the invention can be used to

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CC target drugs to a tumour, in assays to determine biological activity, to
CC raise antibodies/elicit an immune response, to determine quantitative
CC protein levels, as tissue markers, and to isolate receptors or ligands.
CC Polypeptides of the invention may also be useful in treating platelet
CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,
CC ligament and/or nerve tissue, wound healing, treating burns, promoting
CC the proliferation, differentiation and survival of stem cells, as a
CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,
CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
CC fungal infection or from autoimmunity, cancer, allergy, asthma,
CC graft-versus-host disease, eczema, haemophilia, thrombosis,
CC anti-inflammatory diseases, nervous system disorders, and infection.
CC The present sequence represents a protein of the invention.
XX
SQ Sequence 429 AA;
XX
Query Match 83.8%; Score 1146.5; DB 22; Length 429;
Best local similarity 82.9%; Pred. No. 3.6e-109;
Matches 213; Conservative 19; Mismatches 24; Indels 1; Gaps 1;
QY 1 DVLDESEFWDOATGKTFTPLVSODIRDEGMETLEVSNAVKRMWRADSTTKNKLLEYTVQSH 60
DB 174 DVLDDTDAMDATETKFTPLVSODIRDEGMETLEVSNAVKRMWRADSTTKNKLLEYTVQSH 233
QY 61 RESCDTLDISVPPGSKNLPFFVFNDSNGTETKTRDLKEMIGHEOTMLVKTAKNAY 120
DB 234 RKGCDTLDISVPPGSRNLPFFVFNDSNGTETKTRLE-LREMISHEDQSVLTKLSKOGS 292
QY 121 OGAGSEGEELDGYTAVGPIPLARRKSTGASHCQKTSLRVNFEDIGDMSWIIAPKEYD 180
DB 293 TEAGSSHEEDTDGHVAAGSTLARRKRSAGASHCQKTSLRVNFEDIGDMSWIIAPKEYE 352
QY 181 AVECGGCFEPLADDPVPTKHAIVQTLVHLKFTPKYKACCVPTKLSPIISLYKDDMGVP 240
DB 353 AVECGGCFEPLADDPVPTKHAIVQTLVHLKFTPKYKACCVPTKLSPIISLYKDDMGVP 412
QY 241 TLKYHEGMSVAECGCR 257
DB 413 TLKYHEGMSVAECGCR 429

RESULT 6
AAU14431
AAU14431 standard; Protein: 429 AA.
XX
AC AAU14431;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human novel protein #302.
XX
KW Human; novel protein; Antinaemic; osteopathic; antiinflammatory;
KW immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic;
KW anticonvulsant; antiallergic; cerebroprotective; antifungal; antiviral;
KW antibacterial; antiallergic; dermatological; haemostatic; antistimatic;
KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW tissue regeneration; immune disorder.
XX
OS Homo sapiens.
XX
PN WO20015437-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US02623.
XX
PR 25-JAN-2000; 2000US-0491404.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;

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XX WPI: 2001-451939/48.
 DR N-PSDB; AAS22736.
 XX Isolated polypeptides useful for treating anti-inflammatory diseases,
 PT nervous system disorders, and for regenerating bone and cartilage -
 XX Example 4; Page 812-813; 894pp; English.
 XX The invention relates to polynucleotides encoding novel human
 CC proteins or their active domains. The polypeptides, polynucleotides and
 CC antibodies raised against the polypeptides are used in a method of
 CC treatment of a mammal and prevention of disorders caused by the aberrant
 CC protein expression or activity. The polypeptides can be used as
 CC molecular weight markers, food supplements, and in antibody production.
 CC The polypeptides are used to identify compounds which bind to the
 CC polypeptides. Polynucleotides of the invention are used as probes and
 CC primers, for sequencing, for chromosome or gene mapping, in the
 CC production of recombinant proteins, and in generating anti-sense DNA or
 CC RNA and in gene therapy. Polypeptides of the invention can be used to
 CC target drugs to a tumour, in assays to determine biological activity, to
 CC raise antibodies/elicitor an immune response, to determine quantitative
 CC protein levels, as tissue markers, and to isolate receptors or ligands.
 CC Polypeptides of the invention may also be useful in treating platelet
 CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,
 CC ligament and/or nerve tissue, wound healing, treating burns, promoting
 CC the proliferation, differentiation and survival of stem cells, as a
 CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,
 CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
 CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
 CC fungal infection or from autoimmunity, cancer, allergy, asthma,
 CC graft-versus-host disease, eczema, haemophilia, thrombosis,
 CC anti-inflammatory diseases, nervous system disorders, and infection.
 CC The present sequence represents a protein of the invention.
 XX
 SO Sequence 429 AA:
 Query: Match 83.8%; Score 1146.5; DB 22; Length 429;
 Best Local Similarity 82.9%; Pred. No. 3.6e-109;
 Matches 213; Conservative 19; Mismatches 24; Indels 1; Gaps 1;
 QY 1 DVEDESETPMOATGKTFTFLVSODIRDEGMELEVSAAKRWKRVADSTNNKXLEVTYQSH 60
 DB 174 DVLGDGDAMDASNETFTFLVSODIRDEGMELEVSAAKRWKRVADSTNNKXLEVTYQSH 233
 QY 61 RESCDLIDISVPPGSKNLPFVVFVSNDNSNGTKETRLDLKEMIGHDETMVLYKTAKNAV 120
 DB 234 RKCGDIDLISVPPGSKNLPFVVFVSNDNSNGTKETRLDLKEMIGHDETMVLYKTAKNAV 292
 QY 121 QGAGESQEEEGLDGYTAVGPIILARRKSTGASSHOQKSLRVNFEDIGMOSWIAPKEYV 180
 DB 293 TPAEGSSHEEDTDGHAANSTILARRKRSAGASHOQKSLRVNFEDIGMOSWIAPKEYV 352
 QY 181 AYECKGCGCFPLADVTPTKHAIVOTLVHLKPTKVGACVPTKLSISILYKDDMGVP 240
 DB 353 AYECKGCGCFPLADVTPTKHAIVOTLVHLKPTKVGACVPTKLSISILYKDDMGVP 412
 QY 241 TLKYHEGMSVAECGR 257
 DB 413 TLKYHEGMSVAECGR 429
 RESULT 7
 AAR6607
 ID AAR6607 standard; Protein: 427 AA.
 XX
 AC AAR6607;
 XX
 DT 02-AUG-1995 (first entry)
 XX
 DE Dorsalin I.
 XX Dorsalin; neural crest cell differentiation; nerve cells; neurons;

KW regeneration; wound healing; bone growth; tumour; neurofibroma;
 KW Schwann cell tumour.
 XX
 OS Gallus gallus.
 XX
 PN WO9428016-A.
 XX
 PD 08-DEC-1994.
 XX
 PF 20-MAY-1994; 94MO-US05743.
 XX
 PR 20-MAY-1993; 93US-0065844.
 XX
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 PI Basler K, Jessel TM, Yamada T;
 DR WPI: 1995-022710/03.
 DR N-PSDB; AAO80276.
 PT New nucleic acid encoding vertebrate dorsalin-1 - and related
 PT vectors, transformed cells, proteins and antibodies, used e.g. to
 PT regenerate nerve cells, promote bone growth etc.
 XX
 PS Claim 17; Page 66-67; 99pp; English.
 XX
 CC Dorsalin-I is able to stimulate neural crest cell differentiation in
 CC culture. It can be used in vivo to regenerate nerve cells; to
 CC promote bone growth and wound healing; and to treat (inhibit growth
 CC of) neural tumours (specifically neurofibroma or Schwann cell
 CC tumours). Fragments of the coding sequence can be useful as probes
 CC for studying nerve development; for isolating other dorsalin
 CC encoding genes and to locate tissues expressing these genes.
 XX
 SO Sequence 427 AA:
 Query: Match 59.1%; Score 808.5; DB 16; Length 427;
 Best Local Similarity 61.9%; Pred. No. 2.2e-74;
 Matches 161; Conservative 31; Mismatches 59; Indels 9; Gaps 5;
 QY 1 DVEDESETPMOATGKTFTFLVSODIRDEGMELEVSAAKRWKRVADSTNNKXLEVTYQSH 60
 DB 174 DVLGDGDAMDASNETFTFLVSODIRDEGMELEVSAAKRWKRVADSTNNKXLEVTYQSH 232
 QY 61 RESCDLIDISVPPGSKNLPFVVFVSNDNSNGTKETRLDLKEMIGHDETMVLYKTAKNAV 117
 DB 233 RKCGDIDLISVPPGSKNLPFVVFVSNDNSNGTKETRLDLKEMIGHDETMVLYKTAKNAV 291
 QY 118 NAYGAGESQEEEGLDGYTAVGPIILARRKSTGASSHOQKSLRVNFEDIGMOSWIAPKEYV 177
 DB 292 NDSSEEDQEBEAT---ARRPHSKRSKRSIGA-NRRKRSILVNRKEIGMOSWIAPKEYV 347
 QY 178 EYDAYECKGCGCFPLADVTPTKHAIVOTLVHLKPTKVGACVPTKLSISILYKDDMGVP 237
 DB 348 DYEAFECKGCGCFPLADVTPTKHAIVOTLVHLKPTKVGACVPTKLSISILYKDDMGVP 407
 QY 238 GVPTLKYHEGMSVAECGR 257
 DB 408 GVPTLKYHEGMSVAECGR 427
 RESULT 8
 AAR6903
 ID AAR6903 standard; Protein: 150 AA.
 XX
 AC AAR6903;
 XX
 DT 10-MAY-1996 (first entry)
 XX
 DE Human BMP-9 polypeptide.
 XX BMP-9; bone; cartilage; wound healing; liver; tissue repair.

OS	Homo sapiens.	
XX	Key	Location/Qualifiers
XX	Cleavage-site	40..41
XX	FT	/note="proteolytic cleavage site"
XX	FT	Protein
XX	FT	41..150
XX	FT	/label= Mat_protein
XX	PN	MO9533830-A1.
XX	PD	14-DEC-1995.
XX	PF	05-JUN-1995; 95MO-US07084.
XX	PR	06-JUN-1994; 94US-0254353.
XX	PA	(GEMV) GENETICS INST INC.
XX	PI	Celeste AJ, Rosen VA, Song JJ, Thies SR, Wozney JM,
XX	DR	WPI; 1996-040235/04.
XX	DR	N-PSDB; AAT13143.
XX	PT	BMP-9 protein able to induce bone and cartilage formation - also
XX	PT	useful in wound healing, tissue repair and for inducing hepatic
XX	PT	growth and function
XX	PS	Claim 1; Page 45-46; 75pp; English.
XX	CC	Human BMP-9 polypeptide (AAR86903) is the product of a DNA fragment
XX	CC	(AA074084) isolated from a human genomic DNA library. Cleavage of
XX	CC	the polypeptide at the consensus proteolytic processing site
XX	CC	gives a 110-amino acid mature protein that dimerizes to form a
XX	CC	homodimeric, active species. Recombinant BMP-9 can be obt'd. by
XX	CC	expression of the genomic DNA in prokaryotic or eucaryotic hosts.
XX	CC	It has therapeutic applns. in the formation of bone and
XX	CC	cartilage, wound healing and tissue repair.
XX	SO	Sequence 150 AA:
XX	Query Match	46.3%; Score 634; DB 17; Length 150;
XX	Best Local Similarity	92.7%; Pred. NO. 4.4e-57;
XX	Matches 114; Conservative	3; Mismatches 6; Indels 0; Gaps 0;
QY	135	VTANGPLARRKSTGASHCQKTSLRNFEDIGMDSMTIAPKREYDAIECKGCGFFPLAD 194
DB	28	HVAAGSTLARRKRSASAGSHCQKTSLRNFEDIGMDSMTIAPKREYDAIECKGCGFFPLAD 87
QY	195	DVFPTKIAIVQTLVHLKFFPTKVGKACVPTKLSPIISILYKDDMKGVPLKHYEGMSVAEC 254
DB	88	DVFPTKIAIVQTLVHLKFFPTKVGKACVPTKLSPIISILYKDDMKGVPLKHYEGMSVAEC 147
QY	255	GCR 257
DB	148	GCR 150
XX	RESULT 9	
XX	AAV82272	
XX	ID	AAV82272 standard; Protein; 150 AA.
XX	AC	AAV82272;
XX	DT	16-JUN-2000 (first entry)
XX	XX	Human bone morphogenetic protein 9 SEQ ID NO:9.
XX	XX	Bone morphogenetic protein 9; BMP-9; bone defect; cartilage defect;
XX	XX	wound healing; tissue repair; hepatic growth; antifertility;
XX	XX	osteoplastic; antiarthritic; vulnery.
XX	XX	Homo sapiens.

PH	Key	Location/Qualifiers
PT	Peptide	1..40
FT	Protein	/label= signal
FT		41..150
XX		/label= Bone_morphogenetic_protein-9
PN	US6034062-A.	
PD	07-MAR-2000.	
XX		
PF	13-MAR-1997;	97US-0815652.
XX		
PR	13-MAR-1997;	97US-0815652.
XX		
PA	(GEMY) GENETICS INST INC.	
XX		
PI	Thies RS, Song JJ;	
XX		
DR	WPI: 2000-255707/22.	
DR	N-PSDB; AAZ93747.	
XX		
PT	Novel bone-morphogenetic protein (BMP)-9 polypeptides, useful in the treatment of bone and cartilage defects and in wound healing and tissue repair, as well as hepatic growth and function	
PS	Claim 1; Column 45-46; 36pp; English.	
XX		
XX	A method has been developed for decreasing proliferation of kidney or lung epithelial cells, or for inhibiting kidney tubule formation, in a patient. The method comprises administering an amount of a bone morphogenetic protein 9 (BMP-9) protein. BMP-9 polypeptides from the invention may be used to induce bone and cartilage formation or other connective tissue formation, in periodontal disease, in wound healing and tissue repair, hepatic growth and function, and in regulating lung and kidney cell function. The polypeptides can be used for healing of bone fractures, open fracture reduction, improved fixation of artificial joints, tooth repair processes, treatment of osteoporosis and osteoarthritis, and as a dietary supplement or as a component of cell culture media. BMP-9 may also be used for repair and regenerating of liver cells. The BMP-9 polypeptides may also have angiogenic, chemotactic and/or chemottractant properties, and may induce collagen synthesis, fibrosis, differentiation processes, cell proliferative responses, cell adhesion responses, and migration. When dimerized, the BMP-9 polypeptide is expected to demonstrate effects on the production of follicle stimulating hormone (FSH), and so may be used as a contraceptive, as a fertility inducing therapeutic, and for advancing the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals. The present sequence represents human BMP-9.	
XX		
XX	Sequence	150 AA:
XX		
XX	Query Match	46.3%; Score 634; DB 21; Length 150;
XX	Best Local Similarity	92.7%; Pred. No. 4,4e-57;
XX	Matches 114; Conservative	3; Mismatches 6; Indels 0; Gaps 0.
OY	135 YTAGGPLARRKSTGASSHCQKTSIRVNFEDIGDMSWIAPKEYDAYEKGCGCFPLAD	194
DB	28 HVAAGSLFARRKSTGASSHCQKTSIRVNFEDIGDMSWIAPKEYDAYEKGCGCFPLAD	87
OY	195 DWPTFKAIYQTLVHLKPKPKCKACQVPTFKISPIIYLKDDMKVPLTKXHYGSMVAEC	254
DB	88 DWPTFKAIYQTLVHLKPKPKCKACQVPTFKISPIIYLKDDMKVPLTKXHYGSMVAEC	147
OY	255 GCR 257	
DB	148 GCR 150	
XX	RESULT 10	
XX	AAR31374	
XX	ID AAR31374 standard; Protein; 150 AA.	

AC AAR31374;
 DT 24-JUN-1993 (first entry)
 DE Human bone morphogenic protein-9 (BMP-9).
 KW bone formation; cartilage formation; wound healing; tissue repair;
 KW surgery; fracture treatment; periodontal disease; osteoporosis;
 KW increase neuronal survival; transplantation; nerves; nervous system.
 XX Homo sapiens.
 OS
 PN M09300432-A.
 PD 07-JAN-1993.
 XX
 XX 25-JUN-1992; 92MO-US05374.
 PF
 XX 25-JUN-1991; 91US-0720590.
 PR
 XX (GEMV) GENETICS INST INC.
 PA
 PI Celeste AJ, Mozney JW;
 XX WPI: 1993-036379/04.
 DR N-PSDB; AA035244.
 DR
 XX New BMP-9 polypeptide(s) induce bone and cartilage formation -
 PT used for treating osteoporosis and fractures, healing wounds and
 PT increasing neuronal survival
 CC
 XX Example 2; Fig 3; 60pp; English.
 XX
 CC This sequence is human bone morphogenic protein-9. The protein can
 CC be used to induce bone and/or cartilage formation and in wound healing
 CC and tissue repair. It can be used in surgery of the treatment of
 CC fractures, periodontal disease or osteoporosis. The protein can also
 CC increase neuronal survival and can be used in transplantation and
 CC treatment of conditions exhibiting a decrease in neuronal survival.
 XX
 SQ Sequence 150 AA;
 Query Match 45.2%; Score 619; DB 14; Length 150;
 Best Local Similarity 91.1%; Pred. No. 1.3e-53;
 Matches 112; Conservative 2; Mismatches 9; Indels 0; Gaps 0;
 QY 135 YTAGPPLARRRRKSTGASSHCOKTSLRVNFEDIGWDSMTIAPKEYDAVECKGCGFPPLAD 194
 DB 28 HVAAGSTLARRRRKRSAGSGSHCOKTSLRVNFEDIGWDSMTIAPKEYDAVECKGCGFPPLAD 87
 QY 195 DVTFPKAIVQTLVHLKFPYKVGACCVPTKLSPIISILYKDDMGVPTLKHYEGMSVAEC 254
 DB 88 DVTFPKAIVQTLVHLKFPYKVGACCVPTKLSPIISILYKDDMGVPTLKHYEGMSVAEC 147
 QY 255 GCR 257
 DB 148 GCR 150

XX OS Homo sapiens.
 XX PN DE10026713-A1.
 XX PD 06-DEC-2001.
 XX PF 30-MAY-2000; 2000DE-1026713.
 XX PR 30-MAY-2000; 2000DE-1026713.
 XX (SEBA/) SEBALD W.
 XX Sebald W, Nickel J;
 XX WPI: 2002-042559/06.
 DR
 XX New mutein of transforming growth factor-beta superfamily protein,
 PT useful for treating or preventing e.g. ectopic bone formation, competes
 PT for receptor binding
 CC
 PS Disclosure; Fig 6; 54pp; German.
 CC The present invention relates to muteins of a chain of a protein which,
 CC when in the form of a homodimer, has antagonistic or partial agonistic
 CC activity, and where the mutation results in the protein binding with low
 CC affinity to its receptor. The protein is a member of the transforming
 CC growth factor beta (TGFbeta) superfamily. The mutant sequences of the
 CC invention can be used in the treatment of diseases associated with the
 CC overexpression of TGFbeta family proteins, including ectopic bone
 CC formation, psoriasis, muscular atrophy, scar formation, fibrosis and
 CC cirrhosis. The present sequence is the human GDF2 protein.
 XX
 SQ Sequence 110 AA;
 Query Match 43.6%; Score 596; DB 23; Length 110;
 Best Local Similarity 96.4%; Pred. No. 2.3e-53;
 Matches 106; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 148 STGASSHCOKTSLRVNFEDIGWDSMTIAPKEYDAVECKGCGFPPLADVPTKHAIVQTL 207
 DB 1 SAGAGSHCOKTSLRVNFEDIGWDSMTIAPKEYDAVECKGCGFPPLADVPTKHAIVQTL 60
 QY 208 VHLKFPYKVGACCVPTKLSPIISILYKDDMGVPTLKHYEGMSVAECGCR 257
 DB 61 VHLKFPYKVGACCVPTKLSPIISILYKDDMGVPTLKHYEGMSVAECGCR 110

RESULT 12
 AAR66200
 ID AAR66200 standard; Protein; 312 AA.
 AC AAR66200;
 XX
 XX 06-AUG-1995 (first entry)
 DT
 XX
 DE Part of bovine bone morphogenetic protein (BMP)-10.
 XX
 KW Bone morphogenetic protein; BMP; bone formation; cartilage;
 KW periodontal disease; osteoporosis.
 XX
 OS Bos taurus.
 XX
 XX Key location/Qualifiers
 FH Peptide 1..204
 FT /label= part of propeptide
 FT Protein 205..312
 FT /label= mature peptide
 XX
 PN M09426893-A.
 PD 24-NOV-1994.

PF 12-MAY-1994; 94WO-US05290.
 XX
 PR 12-MAY-1993; 93US-0061695.
 XX
 PA (GENW) GENETICS INST INC.
 PI Celeste AJ, Wozney JM;
 PT WPI; 1995-006789/01.
 DR N-PSDB; AA079524.
 XX
 PT New bone morphogenetic protein 10 and related nucleic acid -
 PT vectors and transformed cells, induces formation of cartilage and
 PT bone, useful for healing fractures, wounds, etc., or treating
 PT osteoporosis.
 PS
 PS Disclosure; Page 34-35; 51pp; English.
 XX
 CC BMP-10 is produced by culturing a host cell transformed with a DNA
 CC sequence comprising AA079524 from bps 167 to 1102 or from bps 779-
 CC 1102. A DNA sequence comprising bps 779 or 797-1102 of AA079524 is
 CC claimed. AA079524 is from clone lambda 7r-20 which was derived as
 CC follows. A phage library of bovine genomic DNA was screened (a)
 CC under low stringency conditions with a human BMP-7 cDNA fragment and
 CC (b) under high stringency conditions with BMP-5, -6 and -7 probes.
 CC Once clone positive in the first screen but negative in the second,
 CC lambda 7r-20 (ATCC 75452), was sequenced. It encodes at least of
 CC a portion of bovine BMP-10. The processing of BMP-10 into the mature
 CC form is expected to involve dimerisation and removal of the
 CC N-terminal region. BMP-10 may exist as a homodimer with both
 CC subunits being the 108 AA mature peptides. Alternatively, it may be
 CC a heterodimer with one 108 AA subunit and the other subunit from
 CC any one of BMP 1-9. Fragments derived from clone lambda 7r-20 may
 CC be used to isolate homologous human DNA (see AA079525/R66201, AA079526,
 CC AA079527, AA079531/R66202).
 CC
 XX
 XX
 SQ Sequence 312 AA:
 Query Match 38.0%; Score 519.5; DB 16; Length 312;
 Best Local Similarity 42.8%; Pred. No. 7.6e-45;
 Matches 119; Conservative 43; Mismatches 73; Indels 43; Gaps 10;
 QY 1 DYLEDSEWMDATGATGKTVLSQDI--RDEGNETLEVSAAVKRWVRADSTTNKLEVTYQ 58
 DB 57 EYLESKEDTLGRQQLTDTSAARKHDPILVVFSDQS--SEKEREKELDMIAHEQ---- 113
 QY 59 SHRESQDT-----IDISVPPGSKMLPFVVFVFSNDRSNGTKEFTLDLKEIMIGHEDFTMLV 113
 DB 114 SKHEMDTLGRQQLTDTSAARKHDPILVVFSDQS--SEKEREKELDMIAHEQ---- 166
 QY 114 KTKANAYGAGESQDEEBLDGYTAVGP-----LLARRK-----RSTGASSHCQKTS 159
 DB 167 -----PPEMDNLDLDCYSN-GPGEELLLQMSNNIIYDSTARIRRNANGNCKRPT 215
 QY 160 LAVNFDIGMSWIIAPKEVDAYECRGKGFEPPLADVTPTKNAIVOTLVHLKFPKRVGA 219
 DB 216 LYIDRKEIGMSWIIAPRGVEAYECRGVCNYPVLAHEHLTPTKNAIIQALVHLKNSOKASKA 275
 QY 220 CCVPTKSPISILYKDKMGVPTLKYHNEGMSVAECGCR 257
 DB 276 CCVPTKSPISILYL-DKGVVTKYFKYEGMAVSECGCR 312

KW Bone morphogenetic protein; BMP; bone formation; cartilage;
 KW peridental disease; osteoporosis; primer.
 XX
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT 317..424
 FT Protein /label= mature protein
 XX
 XX MO9426893-A.
 XX
 PD 24-NOV-1994.
 XX
 PF 12-MAY-1994; 94WO-US05290.
 XX
 PR 12-MAY-1993; 93US-0061695.
 XX
 PA (GENW) GENETICS INST INC.
 PI Celeste AJ, Wozney JM;
 PT WPI; 1995-006789/01.
 DR N-PSDB; AA079531.
 XX
 PT New bone morphogenetic protein 10 and related nucleic acid -
 PT vectors and transformed cells, induces formation of cartilage and
 PT bone, useful for healing fractures, wounds, etc., or treating
 PT osteoporosis.
 PS
 PS Claim 18; Page 39-41; 51pp; English.
 XX
 CC AA079525/R66201 comprise the partial human BMP-10 sequence.
 CC An oligo probe based on nts 85-114 of AA079525 was
 CC used to screen a human fetal liver cDNA library. The cDNA of one
 CC of the positively hybridising recombinants, named HFL-3, was
 CC isolated and deposited at the ATCC. A portion of the DNA sequence
 CC in clone HFL-3 is set out in AA079531/R66202. An oligo probe based
 CC on nts 355-384 of AA079531 was used to screen a human genomic
 CC library. The DNA from one of the positively hybridising recombinants,
 CC named 20GEN-3, was isolated and deposited at the ATCC, and a
 CC portion of this clone is set forth in AA079531. A portion of
 CC 20GEN-3 was determined to be identical to cDNA clone HFL-3.
 CC The extent of this overlap is nts 219-316. Nts 1-218 are derived
 CC from genomic clone 20GEN-3 and nts 317-1584 are derived from cDNA
 CC clone HFL-3. Nts 1108 or 1126-1431 are claimed. The purified
 CC mature human BMP-10 polypeptide is also claimed.
 CC
 XX
 XX
 SQ Sequence 424 AA:
 Query Match 37.8%; Score 516.5; DB 16; Length 424;
 Best Local Similarity 42.8%; Pred. No. 2.4e-44;
 Matches 119; Conservative 48; Mismatches 68; Indels 43; Gaps 11;
 QY 1 DYLEDSEWMDATGATGKTVLSQDI--RDEGNETLEVSAAVKRWVRADSTTNKLEVTYQ 58
 DB 169 EYLE-SKQDNBERNMLVLSGELTYGTNSEMFETVDALIRMOKGSST--HOLEVHIE 225
 QY 59 S-HRESQDT-----IDISVPPGSKMLPFVVFVFSNDRSNGTKEFTLDLKEIMIGHEDFTMLV 113
 DB 226 SKHDAEDASSGRLEIDTSAQNKHNPILVIFSDQS--SPKEKEREKELDMIAHEQDLP 282
 QY 114 KTKANAYGAGESQDEEBLDGYTAVGP-----LLARRK-----RSTGASSHCQKTS 159
 DB 283 -----DNLGLDSFSS-GPGEELLLQMSNNIIYDSTARIRRNANGNCKRPT 327
 QY 160 LAVNFDIGMSWIIAPKEVDAYECRGKGFEPPLADVTPTKNAIVOTLVHLKFPKRVGA 219
 DB 328 LYIDRKEIGMSWIIAPRGVEAYECRGVCNYPVLAHEHLTPTKNAIIQALVHLKNSOKASKA 387
 QY 220 CCVPTKSPISILYKDKMGVPTLKYHNEGMSVAECGCR 257
 DB 388 CCVPTKSPISILYL-DKGVVTKYFKYEGMAVSECGCR 424

ID	AA	Residue	Location/Qualifiers
AA92029	standard	Protein, 424 AA.	
AA92029			
19-JUL-2000	(first entry)		
Human bone morphogenic protein-10 (BMP-10).			
human bone morphogenic protein-10; BMP-10; Vg1 growth factor; CKGF; mutant; cystine knot growth factor; hairpin loop; infertility.			
Homo sapiens.			
Key		Location/Qualifiers	
Misc-difference 1..326	/note-	"optionally mutated to increase electrostatic interaction between beta hairpin structure and a receptor"	
Domain	327..353	/label= beta hairpin_loop_1	
	/note=	"mutant optionally comprises one or more substitutions in these residues"	
Misc-difference 354..392	/note-	"optionally mutated to increase electrostatic interaction between beta hairpin structure and a receptor"	
Domain	394..416	/label= beta_hairpin_loop_3	
	/note=	"mutant optionally comprises one or more substitutions in these residues"	
Misc-difference 417..424	/note-	"optionally mutated to increase electrostatic interaction between beta hairpin structure and a receptor"	
WO200017360-A1.			
30-MAR-2000.			
19-MAR-1999;	99MO-US05908.		
22-SEP-1998;	98MO-US19772.		
(UYMA-) UNIV MARYLAND BALTIMORE.			
Weintraub BD, Szkudlinski MW;			
WPI; 2000-283585/24.			
New mutant cystine knot growth factor proteins comprising one or more mutant subunits, useful for treating or preventing diseases e.g. hypothyroidism and thyroid cancer			
Claim 475; Page 310; 320pp; English.			
This is the wild type human bone morphogenic protein-10 (BMP-10).			
Mutants comprise at least one electrostatic charge altering mutation in a beta hairpin loop, resulting in increased bioactivity.			
Mutant cystine knot growth factor (CKGF) proteins comprising one or more mutant subunits and having novel properties or improved pharmacological properties, compared to wild type CKGFs, are claimed. The CKGF superfamily comprises at least four families of growth factors: the glycoprotein hormones, the platelet-derived growth factor (PDGF) family, the neurotrophins and the transforming growth factor-beta family; the families are known to be structurally similar (especially comprising the cystine knot topology) and it was shown that mutations at certain positions in the CKGF hairpin loops of family members and other members of the CKGF superfamily could significantly alter the biological activities of the CKGF.			
Mutant transforming growth factor family proteins or analogues are useful			

CC	for treatment of ovulatory dysfunction, luteal phase defect, unexplained infertility, time-limited conception and in assisted reproduction.
XX	
50	Sequence 424 AA;
	Query Match 37.8%; Score 516.5; DB 21; Length 424; Best Local Similarity 42.8%; Pred. No. 2.4e-44; Matches 119; Conservative 48; Mismatches 68; Indels 43; Gaps 11.
OY	1 DYLEDSTNQATGTCTFLVSDI--RDGEWTELEVSAYKRWVRADSTINKNKLEYVO 58 :: : :::: : :: : :: : :: : :: : :: : :: : :: :
Dd	169 EYVL-SKGDEGERNNMLVSGEITVTNSEWTFPVTAIRMKSSGST-HOLEYHIE 225 :: : :: : :: : :: : :: : :: : :: : :: : :: : :: : :: : :: :
OY	59 S-AHEESCDT----LDISVPGSKNLPFFVFVFENDSNGTKTRDLKKEMIGHQETMIV 113 :: : :: : :: : :: : :: : :: : :: : :: : :: : :: : :: : :: :
Dd	226 SKHEDADASGRLEIDTSAGNKHNPDLVFSDDGS--SDKERREELNEMISHQDEL- 282 :: : :: : :: : :: : :: : :: : :: : :: : :: : :: : :: : :: :
OY	114 KTKANAYOGAGESEOEEDGDGTANGP---ILARRK-----RSTGASSHCQKTS 159 : :: : :: : :: : :: : :: : :: : :: : :: : :: : :: : :: :
Dd	283 -----DNLGLDSPSS-GPGEEALLQMRNSIIYDSTARIRRNKGNVCRTPT 327 : :: : :: : :: : :: : :: : :: : :: : :: : :: : :: : :: :
OY	160 LRVNFEDIGNDSMILAPKEVDYECKGCGFPLADVPTKHAIVOTLVHLKPFTKYGKA 219 :: : :: : :: : :: : :: : :: : :: : :: : :: : :: : :: : :: :
Dd	328 LYDFKEIGDMSNIAPPGVEAEFGCGVGNPYLAHLPRTHALIIQLAVHLKNSQKASKA 387 :: : :: : :: : :: : :: : :: : :: : :: : :: : :: : :: : :: :
OY	220 CCVPTKLSPISILTKDKDMGYPLLKIHYEGMSVAEEGCR 257 :: : :: : :: : :: : :: : :: : :: : :: : :: : :: : :: : :: :
Dd	388 CCVPTKLEPISTLYL-DKGVVYYKFKEEGMAVSEECGR 424 :: : :: : :: : :: : :: : :: : :: : :: : :: : :: : :: : :: :
	RESULT 15
AAOY06304	
ID	AAOY06304 standard; Protein: 421 AA.
AC	
XX	AAOY06304:
DT	31-AUG-1999 (first entry)
XX	
DE	Mouse pancreatic-derived factor PDF1.
XX	
KW	PDP1; pancreatic-derived factor; mouse; signal transduction; transforming growth factor-beta; pancreas; diabetes; therapy; diagnosis.
KM	
XX	
OS	Mus musculus.
XX	
FH	Key Location/Qualifiers
FT	Domain 320..333
FT	/note="core motif"
XX	
FN	W09929719-AZ.
PD	17-JUN-1999.
XX	
PF	09-DEC-1998; 98MO-US26165.
PR	09-DEC-1997; 97US-0069071.
XX	
PA	(ONTO-) ONTOGENY INC.
XX	
PI	Edlund H;
XX	
DR	WPI; 1999-385571/32.
DR	N-PSDB; AAX59115.
XX	
PT	New Isolated pancreatic-derived factor polypeptides used for the treatment of a pancreatic disorder
XX	
PS	Claim 2; Page 82-84; 84pp; English.
XX	
CC	This sequence represents novel mouse pancreatic-derived factor PDF1, as predicted from a cDNA clone (see AAX59115) obtained from fetal pancreatic bud cDNA. PDF1 shows homology to members of the
CC	

CC transforming growth factor-beta superfamily, especially BMP2a.
CC Its expression in the developing pancreas indicates a role in the
CC development of endodermal tissue and in particular in pancreas
CC development. Experimental evidence indicates a functional role
CC in signal transduction mediated by members of the TGF-beta
CC superfamily. PDF1 and PDF2 (see AAY06303) play a role in determining
CC tissue fate and in maintenance of differentiated states. They can
CC be used for the manufacture of medicaments for the treatment of a
CC pancreatic disorder or to modulate growth and/or differentiation of
CC pancreatic cells or stem cells capable of differentiating to
CC pancreatic cells (claimed). PDF polynucleotides, polypeptides and
CC modulator compounds can be used for treating e.g. diabetes, liver
CC disease, various cancers, leukemia, psoriasis, bone disease,
CC fibropoliferative disorders, atherosclerosis, chronic inflammation,
CC Alzheimer's disease, Parkinson's disease, Huntington's chorea,
CC amyotrophic lateral sclerosis, spinocerebellar degeneration,
CC disorders associated with connective tissue, e.g. de-differentiation
CC of chondrocytes or osteocytes, vascular disorders which involve
CC de-differentiation of endothelial tissue and smooth muscle cells,
CC gastric ulcers characterized by degenerative changes in glandular
CC cells, and renal conditions marked by failure to differentiate,
CC e.g. Wilms' tumors, to reform injured tissue, to improve grafting
CC and morphology of transplanted tissue, e.g. PDF agonists and
CC antagonists can be used in a differential manner to regulate
CC different stages of organ repair after physical, chemical or
CC pathological insult, in repair of pancreatic endocrine or exocrine
CC function, cartilage repair, increasing bone density, liver repair
CC subsequent to a partial hepatectomy, or to promote regeneration of
CC lung tissue in the treatment of emphysema. Modulation of the
CC function of PDF can be used in both cell culture and therapeutic
CC methods involving generation and maintenance of beta-cells and
CC possibly also for non-pancreatic tissue, such as in controlling the
CC development and maintenance of tissue from the digestive tract,
CC spleen, lungs, and other organs which derive from the primitive
CC gut. The products can also be used for treating endocrinopathies,
CC sepsis (including malaria), congestive cardiac failure, hepatic and
CC renal insufficiencies, various genetic abnormalities of metabolism,
CC and exogenous toxins (such as alcohol). PDF therapeutics can also
CC be used in the treatment of hyperproliferative vascular disorders,
CC e.g. smooth muscle hyperplasia (such as atherosclerosis) or
CC restenosis, as well as other disorders characterized by fibrosis,
CC e.g. rheumatoid arthritis, insulin dependent diabetes mellitus,
CC glomerulonephritis, cirrhosis, and scleroderma, particularly
CC proliferative disorders in which loss of a TGF-beta autocrine or
CC paracrine signaling is implicated. They can also be used to
CC modulate spermatogenesis and to treat disorders of the female
CC reproductive system which lead to infertility including polycystic
CC ovarian syndrome. The products can also be used for detection,
CC diagnosis and drug screening.
CC
XX
SQ

Sequence 421 AA:

Query Match 37.1%; Score 508; DB 20; Length 421;
Best Local Similarity 42.5%; Pred. NO. 1.8e-43;
Matches 114; Conservative 50; Mismatches 78; Indels 26; Caps 10;

QY 1 DVLDESETDQATGCTKTLVSDI--RDGWELETVSSAVKRWVRADSTINKKLEVVQ 58
DB 169 EVLESADSEER-SMLVLTSTGYTNGNSEWTFVDTATRRMOKSPST--HOLEIHIE 225
QY 59 SHRESCD----TLDISVPGSKNLPEFVVFSDNRNGTKETRLDLLKEMIGHOEIMLV 113
DB 226 SRQNOAEDTGRGOLEIDMSAKNRHPLVVFSDDSN-DKEOK-DELNELITHEODLDD 283
QY 114 KTAANAYOGAGE---SOEEGLDGYTAVGPLLARRKRGSTGASHQCTSLRVNFDIGW 169
DB 284 SDA--FFSGPDEALLOHRSNMIDSSA-----RIRNMAKNYCKKTPLYIDFKEIGW 334
QY 170 DSWIILAREVDAYCKGCGFFPLADVDYPTKHAIVQTLVHLKFTKVGKACCVPTKLSPI 229
DB 335 DSWIILAPGTEAFECRGVCNYPLEALHTPTKHAIIQALVHLKNSOKASKACCVPTKLDPI 394
QY 230 SILYKDDMGVPTLKHYHEGMSVAECCGR 257

DB 395 SILYL-DKGVYTKFKFKEGMASVSECCGR 421

Search completed: April 2, 2003, 14:49:34
Job time : 77 secs